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(54) Title: COMPOSITIONS CONTAINING TUMOR REJECTION ANTIGEN PRECURSORS OR TUMOR REJECTION ANTIGENS, AND AN ADJUVANT AND/OR GROWTH FACTOR

(57) Abstract

Compositions with improved immunogenic effect are disclosed. The compositions contain one or more peptides which, when complexed with a cell surface molecule, such as an MHC, HLA or B cell receptor, provoke an immune response. The compositions contain adjuvants such as saponins, which potentiate the immune response. Especially preferred are compositions which stimulate cytolytic T cell responses, such as peptides which satisfy criteria for MHC binding, such as peptides derived from tumor rejection antigen precursors, including MAGE, BAGE, and GAGE derived peptides.

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COMPOSITIONS CONTAINING TUMOR REJECTION ANTIGEN
PRECURSORS OR TUMOR REJECTION ANTIGENS,
AND AN ADJUVANT AND/OR GROWTH FACTOR

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RELATED APPLICATIONS

This application is a continuation in part of all of the following applications, each of which discuss the provocation of cytolytic T cells in the presence of complexing tumor rejection antigens and MHC/HLA molecules: PCT application PCT/US92/04354 (designating the United States); Serial No. 938,334, filed August 31, 1992; Serial No. 008,446, filed January 22, 1993; Serial No. 54,714, filed April 28, 1993; Serial No. 203,054, filed February 28, 1994; Serial No. 233,305, filed April 26, 1994; Serial No. 195,186, filed February 14, 1994; Serial No. 196,630, filed February 15, 1994; Serial No. 32,978, filed March 18, 1993; Serial Nos. 217,186; 217,187; and 217,188, all of which were filed on March 24, 1994; Serial No. 190,411, filed on April 1, 1994 and Serial No. 253,503, filed June 3, 1994.

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FIELD OF THE INVENTION

This invention relates to compositions useful in the generation of an immune response against the classes of molecules referred to as tumor rejection antigen precursors ("TRAPs") and tumor rejection antigens ("TRAs"). The immune response includes, *inter alia*, the production of antibodies against the TRAPs and TRAs, as well as T cells specific for complexes of TRA and major histocompatibility molecules ("MHCs"). Such T cells and antibodies may be generated, e.g., in a mouse, rat, rabbit, sheep, goat or other non-human animal, and then used in diagnostic methods to identify tumor presence. The compositions may also be used, therapeutically, via administration to a subject afflicted with a cancerous condition or one where cell transformation has taken place, such as melanoma or dysplastic nevi, to provoke an

5 immune response against tumors, cancer cells, and transformed
cells.

BACKGROUND AND PRIOR ART

10 The study of the recognition or lack of recognition of
cancer cells by a host organism has proceeded in many
different directions. Understanding of the field presumes
some understanding of both basic immunology and oncology.

15 Early research on mouse tumors revealed that these
displayed molecules which led to rejection of tumor cells when
transplanted into syngeneic animals. These molecules are
"recognized" by T-cells in the recipient animal, and provoke
a cytolytic T-cell response with lysis of the transplanted
cells. This evidence was first obtained with tumors induced
in vitro by chemical carcinogens, such as methylcholanthrene.
20 The antigens expressed by the tumors and which elicited the T-
cell response were found to be different for each tumor. See
Prehn, et al., J. Natl. Canc. Inst. 18: 769-778 (1957); Klein
et al., Cancer Res. 20: 1561-1572 (1960); Gross, Cancer Res.
3: 326-333 (1943), Basombrio, Cancer Res. 30: 2458-2462 (1970)
25 for general teachings on inducing tumors with chemical
carcinogens and differences in cell surface antigens. This
class of antigens has come to be known as "tumor specific
transplantation antigens" or "TSTAs". Following the
observation of the presentation of such antigens when induced
30 by chemical carcinogens, similar results were obtained when
tumors were induced in vitro via ultraviolet radiation. See
Kripke, J. Natl. Canc. Inst. 53: 333-1336 (1974).

35 While T-cell mediated immune responses were observed for
the types of tumor described supra, spontaneous tumors were
thought to be generally non-immunogenic. These were therefore
believed not to present antigens which provoked a response to
the tumor in the tumor carrying subject. See Hewitt, et al.,
Brit. J. Cancer 33: 241-259 (1976).

40 The family of tumor antigen presenting cell lines are
immunogenic variants obtained by mutagenesis of mouse tumor
cells or cell lines, as described by Boon et al., J. Exp. Med.

5 152: 1184-1193 (1980), the disclosure of which is incorporated by reference. To elaborate, tum⁺ antigens are obtained by mutating tumor cells which do not generate an immune response in syngeneic mice and will form tumors (i.e., "tum⁺" cells). When these tum⁺ cells are mutagenized, they are rejected by
10 syngeneic mice, and fail to form tumors (thus "tum⁻"). See Boon et al., Proc. Natl. Acad. Sci. USA 74: 272 (1977), the disclosure of which is incorporated by reference. Many tumor types have been shown to exhibit this phenomenon. See, e.g., Frost et al., Cancer Res. 43: 125 (1983).

15 It appears that tum⁺ variants fail to form progressive tumors because they elicit an immune rejection process. The evidence in favor of this hypothesis includes the ability of "tum⁻" variants of tumors, i.e., those which do not normally form tumors, to do so in mice with immune systems suppressed
20 by sublethal irradiation, Van Pel et al., Proc. Natl. Acad. Sci. USA 76: 5282-5285 (1979); and the observation that intraperitoneally injected tum⁺ cells of mastocytoma P815 multiply exponentially for 12-15 days, and then are eliminated in only a few days in the midst of an influx of lymphocytes and macrophages (Uyttenhove et al., J. Exp. Med. 152: 1175-
25 1183 (1980)). Further evidence includes the observation that mice acquire an immune memory which permits them to resist subsequent challenge to the same tum⁺ variant, even when immunosuppressive amounts of radiation are administered with
30 the following challenge of cells (Boon et al., Proc. Natl. Acad. Sci. USA 74: 272-275 (1977); Van Pel et al., supra; Uyttenhove et al., supra). Later research found that when spontaneous tumors were subjected to mutagenesis, immunogenic variants were produced which did generate a response. Indeed,
35 these variants were able to elicit an immune protective response against the original tumor. See Van Pel et al., J. Exp. Med. 157: 1992-2001 (1983). Thus, it has been shown that it is possible to elicit presentation of a so-called "tumor rejection antigen" in a tumor which is a target for a
40 syngeneic rejection response. Similar results have been obtained when foreign genes have been transfected into

5 spontaneous tumors. See Fearson et al., Cancer Res. 48: 2975-1980 (1988) in this regard.

A class of antigens has been recognized which are presented on the surface of tumor cells and are recognized by cytotoxic T cells, leading to lysis. This class of antigens 10 will be referred to as "tumor rejection antigens" or "TRAs" hereafter. TRAs may or may not elicit antibody responses. The extent to which these antigens have been studied, has been via cytolytic T cell characterization studies in vitro i.e., the study of the identification of the antigen by a particular 15 cytolytic T cell ("CTL" hereafter) subset. The subset proliferates upon recognition of the presented tumor rejection antigen, and the cells presenting the antigen are lysed. Characterization studies have identified CTL clones which specifically lyse cells expressing the antigens. Examples of 20 this work may be found in Levy et al., Adv. Cancer Res. 24: 1-59 (1977); Boon et al., J. Exp. Med. 152: 1184-1193 (1980); Brunner et al., J. Immunol. 124: 1627-1634 (1980); Maryanski et al., Eur. J. Immunol. 124: 1627-1634 (1980); Maryanski et al., Eur. J. Immunol. 12: 406-412 (1982); Palladino et al., 25 Canc. Res. 47: 5074-5079 (1987). This type of analysis is required for other types of antigens recognized by CTLs, including major histocompatibility antigens, the male specific H-Y antigens, and a class of antigens, referred to as "tum-" antigens, and discussed herein.

30 A tumor exemplary of the subject matter described supra is known as P815. See DePlaen et al., Proc. Natl. Acad. Sci. USA 85: 2274-2278 (1988); Szikora et al., EMBO J 9: 1041-1050 (1990), and Sibille et al., J. Exp. Med. 172: 35-45 (1990), the disclosures of which are incorporated by reference. The 35 P815 tumor is a mastocytoma, induced in a DBA/2 mouse with methylcholanthrene and cultured as both an *in vitro* tumor and a cell line. The P815 line has generated many tum⁻ variants following mutagenesis, including variants referred to as P91A (DePlaen, supra), 35B (Szikora, supra), and P198 (Sibille, 40 supra). In contrast to tumor rejection antigens - and this is a key distinction - the tum⁻ antigens are only present after

5 the tumor cells are mutagenized. Tumor rejection antigens are present on cells of a given tumor without mutagenesis. Hence, with reference to the literature, a cell line can be tum⁺, such as the line referred to as "P1", and can be provoked to produce tum⁻ variants. Since the tum⁻ phenotype differs from that of the parent cell line, one expects a difference in the DNA of tum⁻ cell lines as compared to their tum⁺ parental lines, and this difference can be exploited to locate the gene of interest in tum⁻ cells. As a result, it was found that genes of tum⁻ variants such as P91A, 35B and P198 differ from their normal alleles by point mutations in the coding regions 10 of the gene. See Szikora and Sibille, supra, and Lurquin et al., Cell 58: 293-303 (1989). This has proved not to be the case with the TRAs of this invention. These papers also demonstrated that peptides derived from the tum⁻ antigen are 15 presented by the L^d molecule for recognition by CTLs. P91A is presented by L^d, P35 by D^d and P198 by K^d.

Prior patent applications PCT/US92/04354, U.S. Serial No. 20 807,043; 764,364; 728,838 and 705,702, all of which are incorporated by reference and U.S. Patent No. 5,342,774, 25 describe inventions involving, *inter alia*, genes and other nucleic acid molecules which code for various TRAPs, which are in turn processed to tumor rejection antigen, or "TRAs". SEQ ID NOS: 1-26 which are a part of the subject application present sequences of genes coding for various TRAPs, and the 30 TRA referred to hereafter as MZ2E, which is derived from MAGE-1 TRAP (SEQ ID NO: 26).

The genes are useful as a source for the isolated and 35 purified tumor rejection antigen precursor and the TRA themselves, either of which can be used as an agent for treating the cancer for which the antigen is a "marker", as well as in various diagnostic and surveillance approaches to oncology, discussed infra. It is known, for example, that tum⁻ cells can be used to generate CTLs which lyse cells 40 presenting different tum⁻ antigens as well as tum⁺ cells. See, e.g., Maryanski et al., Eur. J. Immunol. 12: 401 (1982); and van den Eynde et al., Modern Trends in Leukemia IX (June

5 1990), the disclosures of which are incorporated by reference. The tumor rejection antigen precursor may be expressed in cells transfected by the gene, and then used to generate an immune response against a tumor of interest.

10 In the parallel case of human neoplasms, it has been observed that autologous mixed lymphocyte-tumor cell cultures ("MLTC" hereafter) frequently generate responder lymphocytes which lyse autologous tumor cells and do not lyse natural killer targets, autologous EBV-transformed B cells, or autologous fibroblasts (see Anichini et al., Immunol. Today 8: 15 385-389 (1987)). This response has been particularly well studied for melanomas, and MLTC have been carried out either with peripheral blood cells or with tumor infiltrating lymphocytes. Examples of the literature in this area including Knuth et al., Proc. Natl. Acad. Sci. USA 81: 2804-20 2802 (1984); Mukherji et al., J. Exp. Med. 158: 240 (1983); Hérin et all, Int. J. Canc. 39: 390-396 (1987); Topalian et al, J. Clin. Oncol 6: 839-853 (1988). Stable cytolytic T cell 25 clones have been derived from MLTC responder cells, and these clones are specific for the tumor cells. See Mukherji et al., supra, Hérin et all, supra, Knuth et al., supra. The antigens recognized on tumor cells by these autologous CTLs do not appear to represent a cultural artifact, since they are found on tumor cells *in vivo*. Topalian et al., supra; Degiovanni et al., Eur. J. Immunol. 20: 1865-1868 (1990). These 30 observations, coupled with the techniques used herein to isolate the genes for specific murine tumor rejection antigen precursors, have led to the isolation of nucleic acid sequences coding for tumor rejection antigen precursors of TRAs presented on human tumors. It is now possible to isolate 35 the nucleic acid sequences which code for tumor rejection antigen precursors, including, but not being limited to those most characteristic of a particular tumor, with ramifications that are described infra.

40 Additional work has focused upon the presentation of TRAs by the class of molecules known as major histocompatibility complexes, or "MHCs". Human forms of these molecules are

5 "human leukocyte antigens" or "HLAs". This work has resulted
in several unexpected discoveries regarding the field.
Specifically in U.S. patent application Serial Number 938,334,
now U.S. Patent No. _____ the disclosure of which is
10 incorporated by reference, nonapeptides are taught which are
presented by the HLA-A1 molecule. The reference teaches that
given the known specificity of particular peptides for
particular HLA molecules, one should expect particular
peptides to bind one HLA molecule. These peptides, presented
15 herein as SEQ ID NOS: 27-34 are also presented in Traversari
et al., J. Exp. Med. 176: 1453-1457 (1992). This is
important, because different individuals possess different HLA
phenotypes. As a result, while identification of particular
peptides or of particular motifs, and the peptides which are
20 members thereof, as being partners for a specific HLA molecule
has diagnostic and therapeutic ramifications, these are only
relevant for individuals with that particular HLA phenotype.
There is a need for further work in the area, because cellular
abnormalities are not restricted to one particular HLA
25 phenotype, and targeted therapy requires some knowledge of the
phenotype of the abnormal cells at issue.

In U.S. Patent Application Serial Number 008,446, filed
January 22, 1993 and incorporated by reference, the fact that
the MAGE-1 expression product is processed to a second TRA is
disclosed. This second TRA is presented by HLA-Cw* 1601
30 molecules. The disclosure shows that a given TRAP can yield
a plurality of TRAs.

In U.S. Patent Application Serial Number 994,928, filed
December 22, 1992, and incorporated by reference herein,
tyrosinase is described as a tumor rejection antigen
precursor. This is a well known molecule as per Kwon, U.S.
35 Patent No. 4,898,814. This reference discloses that a
molecule which is produced by some normal cells (e.g.,
melanocytes), is processed in tumor cells to yield a tumor
rejection antigen that is presented by HLA-A2 molecules. The
40 peptide presented thereby is described in U.S. Application
Serial No. 54,714, filed April 28, 1993. SEQ ID NO: 35 sets

5 forth this peptide. Additional tyrosinase derived peptides presented by HLA molecules are set forth in Serial Nos. 203,054, and 233,305 filed February 28, 1994 and April 26, 1994 and incorporated by reference (SEQ ID NOS: 36-41).

10 Other peptides which are TRAs are described in additional patent applications. U.S. Patent Application Serial No. 195,186, filed February 14, 1994, and incorporated by reference herein, sets forth three peptides (SEQ ID NOS: 42-44 herein), which are derived from MAGE-1 and which complex with HLA-Cw⁺ 1601. Serial No. 196,630, filed February 15, 1994, 15 discloses an unrelated tumor rejection antigen precursor, the so-called "BAGE" gene, and peptides derived therefrom, which are processed and then presented by HLA-Cw⁺ 1601. These are set forth as SEQ ID NOS: 45-48, and this application is incorporated by reference. SEQ ID NO: 48 is the tumor 20 rejection antigen. Additional coding sequences for a tumor rejection antigen precursor are set forth in Serial No. 32,978, filed March 18, 1993 and incorporated by reference. These are included herein as SEQ ID NOS: 49 and 50. A more extended sequence for this gene is set forth in Serial No. 25 272,351, filed July 8, 1994 incorporated by reference, and is SEQ ID NO: 51. In Serial No. 96,039, filed July 22, 1993, the sequence of tumor rejection antigen precursor GAGE is set forth. See SEQ ID NO: 52 for this information.

30 A series of peptides which provoke lysis by cytolytic T cells when presented by MHC molecules are set forth in Serial No. 217,186, Serial No. 08/217,188, and Serial No. 217,187, all filed on March 24, 1994, and all of which are incorporated by reference herein. The first of these applications discloses MAGE-3 derived peptides presented by HLA-A2. Five 35 peptides are of interest. These are repeated here as SEQ ID NOS: 53-57. The second application presents 11 sequences derived from MAGE-2, believed to complex with HLA-A2.1 molecules (SEQ ID NOS: 58-68). The last of these applications discloses two additional peptides (SEQ ID NOS: 69 and 70) 40 derived from MAGE-3 which complex to HLA-A2. Serial No. 190,411, filed April 1, 1994 and incorporated by reference,

5 sets forth three peptides (SEQ ID NO: 71-73), derived from
MAGE-1, which are immunogenic in that they provoke production
of antibodies in a host animal to which they have been
administered. Serial No. 253,503, filed June 3, 1994 and
10 incorporated by reference, teaches a further tumor rejection
antigen precursor gene (SEQ ID NO:74), and a peptide, derived
therefrom (SEQ ID NO:75), which is presented by HLA-B44
molecules. Further in the application of Coulie, Ikeda and
Boon-Falleur, filed concurrently, a sequence coding for a
15 tumor rejection antigen precursor known as DAGE (SEQ ID NO:76)
is set forth. DAGE is found almost universally on tumor
cells, and only on testis cells with respect to normal cell
expression. This makes it especially useful for cancer
diagnosis and in the applications disclosed herein. The above
20 listing should not be presumed to be exhaustive of the TRAP
and TRA literature, but is presented to show its diversity and
the fact that these materials not only provoke T cell
proliferation, but also stimulate production of antibodies.
It is well known that antibody producing cells can be used as
25 a source to produce hybridomas, which in turn produce
monoclonal antibodies. Thus, when the term "antibodies" is
used herein, it encompasses both polyclonal and monoclonal
antibodies.

30 The parent applications to the present case, including
Serial No. 142,368 and Serial No. 190,411, both discuss the
usefulness of combining TRAPs or TRAs with various materials
as adjuvants, to produce vaccines, immunogenic compositions,
etc. Adjuvants, broadly defined, are substances which promote
35 immune responses. Frequently, the adjuvant of choice is
Freund's complete adjuvant, or killed B. pertussis organisms,
used in combination with alum precipitated antigen. A general
discussion of adjuvants is provided in Goding, Monoclonal
Antibodies: Principles & Practice (Second edition, 1986), at
40 pages 61-63, which are incorporated by reference herein.
Goding notes, however, that when the antigen of interest is of
low molecular weight, or is poorly immunogenic, coupling to an
immunogenic carrier is recommended. Such molecules, according

5 to Goding, generally have molecular weights below about 1000. Among the carriers suggested by Goding, at page 283, are keyhole limpet hemocyanin, bovine serum albumin, ovalbumin, and fowl immunoglobulin.

10 What is problematic about such carriers, however, is that frequently they are also immunogenic themselves. Thus, the immune response may be a general one, with part, most, or all of it being directed against the carrier molecule rather than the immunogen itself.

15 Exemplary of developments in the art as they relate to adjuvants is U.S. Patent No. 5,057,540 to Kensil, et al, the disclosure of which is incorporated by reference herein. Kensil et al disclose the preparation of various saponin extracts, which are useful as adjuvants in immunogenic compositions. As natural products, the extracts are not 20 completely defined. Kensil, et al do provide a complete and enabling disclosure for how various extracts, including QA-7, QA-19, and QA-21 (also referred to as QS-21) are prepared. Experiments are set forth in which bovine serum albumin 25 ("BSA") was combined with various extracts (examples 8 and 9), and where feline leukemia virus recombinant glycoprotein "gp70RΔ was tested, following absorption to aluminum hydroxide (alum). The two immunogens tested, however, are expected to be immunogenic in their own right (gp70RΔ has a molecular weight of 70 kd, and serum albumin has about the same 30 molecular weight). No experiments were carried out at all on molecules which should, per se, be considered to be poorly or even non-immunogenic, and thus would be expected to require the use of alum absorption or the use of haptenic carriers for provocation of a response.

35 In PCT Application WO9219758, which corresponds to defensive publication 7697275, which is incorporated by reference herein, an adjuvant referred to as "MTP-MF59" is disclosed. This adjuvant is used in connection with a Plasmodium falciparum protein, "Pfs-25-B". This combination 40 is described as a transmission blocking vaccine. The P. falciparum protein is itself large enough to be immunogenic.

5 Thus, none of the art shows that the improved adjuvants can be used in combination with presumptively non-immunogenic proteins and peptides to yield immunologically effective compositions. This is especially true for TRAP and TRA molecules, as outlined supra.

10 It has now been found, surprisingly, that compositions comprising tumor rejection antigen precursors or tumor rejection antigens can be made which, when administered to a subject animal, provoke an immunogenic response. In especially preferred embodiments the immunogenic portion of the composition consists of TRAP or, more preferably TRA molecules, of one or more types, and an adjuvant. Especially preferred are compositions where the adjuvant is QS21, as is disclosed in the Kensil, et al patent, incorporated by reference supra.

15 20 The immunogens of this invention consist of TRAPs or TRAs, meaning that they do not include haptens, carriers, precipitated alum, or any of the materials normally associated with materials which are or are expected to be poorly immunogenic. In especially preferred embodiments, the compositions consist essentially of the immunogen and the adjuvant.

25 The invention is described in greater detail in the disclosure which follows.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Example

30 35 The following example demonstrates the use of peptide MZ2E (SEQ ID NO: 26) in connection with adjuvant QS-21. It is to be understood, however, that one may routinely substitute proteins or peptides (the first component of the composition) and adjuvants (the second component of the composition). The unexpected effect of the combination of MZ2E and QS21 should occur in the alternate combinations, i.e., when other peptides are used.

40 Subjects tested are patients with stage IV melanoma or high risk stage III malignant melanoma. Stage IV patients have a median survival time of one year following diagnosis,

5 and only a 15% chance of long-term survival (Balch, et al.,
Cutaneous Melanoma, J.b. Lippincott, Philadelphia, 1992). The
standard therapy for these patients includes treatment with
decarbazine or drug combinations with decarbazine; however,
response rates only range from 8-25%, and there is no evidence
of the treatment extending survival. Balch et al., supra.
10 Patients with high risk Stage III melanoma (pT4 thick truncal
primary tumors or extremity melanomas, with five or more
positive regional lymph nodes) have a median survival of 1-2
years following onset, and a 19% chance of long term survival.
15 Balch, et al., supra.

Twelve patients are used in the study, all of whom have either Stage IV or high risk Stage III malignant melanoma in accordance with the criteria provided supra, confirmed by review of histology.

20 The patients fulfil the following additional criteria:

- (i) complete recovery from surgery;
- (ii) no chemotherapy or immunotherapy, within the four weeks preceding immunization;
- (iii) expected survival of at least three months;
- (iv) Karnofsky Performance Status of 60 or more;
- (v) Laboratory results as follows:
 - granulocytes \geq 2,500/min³
 - lymphocytes \geq 700/min³
 - platelets \geq 100,000/min³
 - serum creatinine \leq 2.0 mg/100 ml
 - serum bilirubin \leq 2.0 mg/100 ml
- (vi) for MZ2E immunization, patients are positive for HLA-A1;
- (vii) for MZ2E immunization, the patients' tumors express MAGE-1;
- (viii) they be over 19 years old and be capable of giving informed consent in writing.

40 Any potential subjects who satisfy any of the following
criteria are excluded:

(i) clinically significant heart disease;

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5 (ii) other serious illness, such as active infection
requiring antibiotics, or bleeding disorders;

(iii) treatment with antihistamines, N-SAIDS, or corticosteroids;

10 (iv) immunodeficiency, splenectomy, or radiation therapy
to the spleen;

(v) pregnancy or lactation;

(vi) women of childbearing age who do not use effective methods of contraception.

15 All subjects are treated as outpatients. They are immunized, subcutaneously, with MZ2E (30 ug or 300 ug) and QS21 (100 ug), in 0.3 ml phosphate buffered saline, pH 7.4. Six patients receive 30 ug of peptide, and six receive 300 ug. The first injection is into the deltoid region of the anterior aspect of
20 the thigh, and the site of injection is changed with follow up injections. No injections are given into limbs where draining lymph nodes have been surgically removed or irradiated.

Injections are given at day 1, and then at days 8, 15, 22, and 57. Patients are monitored over a course of 12 weeks, unless intervention is required (as determined by the investigator). Any patients who show stabilization or tumor response remain in the study until disease progression is evidenced. Patients may also be removed from the study or receive different doses of the peptide, if toxicity reactions are observed.

The patients show response as follows. In a complete response, all signs, symptoms, biochemical and imaging evidence of tumor disappear for a period of at least 30 days. In a partial response, there is a decrease in size of all measurable tumors of at least 50% of the sum of products of the greatest and perpendicular diameters for at least 30 days, without the appearance of new lesions or progression of any new lesions. In a minor response, there is a decrease in size of all measurable tumors of at least 25% of the sum of products of greatest and perpendicular diameters, for at least 30 days, without appearance of new lesions or progression of

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5 any lesion. In stable disease, there is a change of less than 25% of the sum of products of greatest and perpendicular diameters, for at least 30 days, without the appearance of new lesions or progression of lesions. In progression of the disease, there is appearance of new tumors, or an increase in 10 the size of measurable tumors of at least 50% of the sum of the product of greatest and perpendicular diameter.

The foregoing example demonstrates a composition comprising an amount of a tumor rejection antigen, i.e., MZ2E, and an adjuvant, i.e., QS21, and the use of the composition in 15 the in vivo treatment of cancer (i.e., melanoma). The tumor rejection antigen is used in an amount sufficient to provoke an immune response against tumor cells which present it on their surface.

20 The compositions of the invention comprise any tumor rejection antigen precursor ("TRAP") or tumor rejection antigen ("TRA"), in combination with a pharmaceutically acceptable adjuvant. Preferred embodiments of the invention utilize the TRAPs and TRAs discussed supra and set forth in SEQ ID NO: 65, as well as the adjuvants described in the 25 Background section.

As will be seen from the foregoing discussion, an important aspect of the invention is stimulation of proliferation of T cells. This can be an initial stimulation or an augmentation of a prior stimulation. In particular, it 30 is desirable to stimulate cytolytic T cells which present peptides, such as the TRAs described herein, on their surfaces. The cytolytic T cells recognize these complexes of MHC and peptide, bind thereto via their receptor, and proliferate. They also lyse the recognized cells. This 35 response can be used not only in vivo, but in vitro, as it is well established that cytolytic T cells specific for particular complexes of MHC and peptide are present in the blood of subjects who have experienced cell transformation. By contacting a blood sample of individuals in vitro with the 40 peptide of interest and cells which present the MHC molecule of interest, any cytolytic T cells in the blood sample will

5 expand, i.e., proliferate. This proliferation can be measured via any of the well known assays designed therefor. Especially preferred are the radioactive chromium (⁵¹Cr) release assay, and the measurement of release of tumor necrosis factor (TNF).

10 The compositions are also useful as stimulators of B cell proliferation, or antibody production. Again, it is well known that B cells produce antibodies, and the size of their targets are well within the sizes of the tumor rejection antigens, and certainly the tumor rejection antigen precursors. As with T cells, the stimulation may be "ab initio", or an augmentation of a prior response, in vitro or in vivo.

15 The amount of TRAP or TRA used will vary, depending upon the purpose of the immunization and the subject to which it is administered. For example, in the case of generating murine antibodies which can then be used, e.g., to diagnose for the presence of cancer cells presenting a TRA, the amount of protein or peptide may be less than that used in a course of in vivo therapy, such as that described in the example, supra. 20 In general, a preferred dose can range from about 1 ug to about 750 ug of protein or peptide per dose. In a preferred embodiment, the range is from about 10 ug to about 500 ug. Most preferably, anywhere from about 30 ug to about 300 ug per dose may be used. Of course, in the context of the therapeutic aspect of the invention, the investigator will 25 modify the dose, as a six month old infant will require dosing different from a full grown man, e.g. The mode of administration may vary, with preferred forms being oral, subcutaneous, intramuscular, intravenous and intraperitoneal 30 administration.

35 The choice of TRAP or TRA protein or peptide in the composition will depend upon parameters determinable by the artisan. It is art recognized, for example, that different TRAs are presented by the various MHC molecules. As such, if 40 a subject is typed, using well known techniques, as presenting HLA-A2 molecules on the surface of tumor cells, one will use

5 a TRA presented by HLA-A2 molecules rather than one presented by, e.g., HLA-Cw* 1601. Similarly, using techniques such as polymerase chain reaction ("PCR"), lysis studies, and other assay methodologies which are well known in the art, one can determine which tumor rejection antigen precursor gene or
10 genes are being expressed by a subject patient. This will lead to the decision as to what protein or peptide to use. Again, by way of example, if a subject's tumor cells are expressing MAGE-3 but not MAGE-1, the peptide used in immunization should be derived from MAGE-3, and not MAGE-1.

15 While the molecules discussed herein are referred to as "tumor" rejection antigens and "tumor" rejection antigen precursors, it is intended that their use, in a therapeutic and also a diagnostic context, extends beyond cancer *per se*. The art is familiar with pathological conditions, such as
20 displastic nevis, which are not cancer *per se*, but where the cells of the afflicted individuals are in fact characterized by transformation. Any and all such conditions are within the intended ambit of the invention.

25 Other aspects of the invention will be clear to the skilled artisan and need not be reiterated here.

30 The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, it being recognized that various modifications are possible within the scope of the invention.

5

(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon-Falleur, Thierry; van den Eynde, Benôit; van der Bruggen, Pierre

10 (ii) TITLE OF INVENTION: COMPOSITIONS CONTAINING TUMOR REJECTION ANTIGEN PRECURSORS OR TUMOR REJECTION ANTIGENS, AND AN ADJUVANT AND/OR GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 76

15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felfe & Lynch
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(E) COUNTRY: USA
20 (F) ZIP: 10022

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
25 (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
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(C) CLASSIFICATION: 435

30 (vii) PRIOR APPLICATION DATA:
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(B) FILING DATE: 22-MAY-1992

(viii) PRIOR APPLICATION DATA:
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35 (B) FILING DATE: 31-AUGUST-1992

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40 (B) FILING DATE: 28-APRIL-1993

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(A) APPLICATION NUMBER: 08/196,630
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(A) APPLICATION NUMBER: 08/032,978
(B) FILING DATE: 18-MARCH-1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,186
(B) FILING DATE: 24-MARCH-1994

25 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,187
(B) FILING DATE: 24-MARCH-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,188
(B) FILING DATE: 24-MARCH-1994

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(A) APPLICATION NUMBER: 08/190,411
(B) FILING DATE: 1-APRIL-1994

30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/253,503
(B) FILING DATE: 3-JUNE-1994

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(ix) TELECOMMUNICATION INFORMATION:
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19

5 (2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGCA AGTTCCGCCT ACAGCTCTAG 180
CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAAGTCTTC CTTATAGAAG TCTTCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTT GCTCTCCAG CATGCATTGT 360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
TATCTTAACT TAGCTCGGT TCCTGCTGGT ACCCTTTGTG CC 462

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: since

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

5 10 15

CAC CCT GAT CGG AAC TCC AAC TTA TTC GAC CGG TAC TCC CTG GAA 86

Asp-Gly-Asp-Gly-Asp-Ang-Sys-Asp-Lys-Lys-His-Arc-Tyr-Ser-Leu-Glu

20 25 30

40 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr

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5	35	40	45	
	AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG	192		
	Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln			
	50	55	60	
	TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC	240		
10	Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser			
	65	70	75	80
	TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC	288		
	Ser Val Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr			
	85	90	95	
15	GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336		
	Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp			
	100	105	110	
	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG	384		
	Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu			
20	115	120	125	
	GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432		
	Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met			
	130	135	140	
	GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480		
25	Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys			
	145	150	155	160
	AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528		
	Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe			
	165	170	175	
30	CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576		
	Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys			
	180	185	190	
	GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG	624		
	Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu			
35	195	200	210	
	GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672		
	Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro			
	220	225	230	235
40	TAG			675

5

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

10

15

GCATGCAGTT GCAAAGCCCA	GAAGAAAGAA ATGGACAGCG	GAAGAAGTGG TTGTTTTTT	60
TTCCCCTTCA TTAATTTCT	AGTTTTAGT AATCCAGAAA	ATTTGATTTT GTTCTAAAGT	120
TCATTATGCA AAGATGTCAC	CAACAGACTT CTGACTGCAT	GGTGAACCTT CATATGATAC	180
ATAGGATTAC ACTTGTACCT	GTTAAAAATA AAAGTTGAC	TTGCATAC	228

20

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

30

35

40

ACACACAGGAG AATGAAAAGA	ACCCGGGACT CCCAAAGACG	CTAGATGTGT	50
GAAGAGATCCTG ATCACTCATT	GGGTGCTCTGA GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT	CTCGTGGGGG GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTGCA AGTTCGCGCT	ACAGCTCTAG CTTGTGAATT	TGTACCCCTT	200
CACGTAAAAAA AGTAGTCCAG	AGTTTACTAC ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGTG TGCTGAGTTT	AGAAGTCTTC CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG	AGGGAGGGACC CCCCCCCTTT	GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA	TTGCACTGAG CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT	TATCTTAACT TAGCTCGGCT	TCCTGCTGGT	450
ACCCCTTG TG CC			462
ATG TCT GAT AAC AAG CCA	GAC AAA GCC CAC AGT	GGC TCA	504

5	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
10	GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC	756
	GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
15	GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
	TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
	AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
	GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
	GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
20	TAG	1137
	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
	TTGTTTTTTT TTCCCCCTCA TTAATTTCT AGTTTTAGT AATCCAGAAA	1237
	ATTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
	CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
25	GTAAAAAATA AAAGTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

	ACACACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCACTCCCT	100
40	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
	AAGTTTGCA AGTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200

5	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCTCCCA CCTCGTCTG TGCTGAGTT AGAAGTCTTC CTTATAGAAG TCTTCGTAT AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCAG CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	250 300 350 400 450
10	ACCCTTTGTG CC ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	462 504 546 588 630
15	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	672 714 756 798
20	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTA	840 882 916 966
25	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC CCCCACTCCT TGCTCCGCTC TCTTCTCTT TCCCACCTTG CCTCTGGAGC	1016 1066 1116
30	TTCAGTCCAT CCTGCTCTGC TCCCTTCCCC CTTTGCTCTC CTTGCTCCCC TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCCTC TTCAGGCTTC CCCATTGCT CCTCTCCCAGA AACCCCTCCCC TTCTGTTCC CCTTTTCGCG CCTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTACCTT	1166 1216 1266 1316
35	TCACCAGCTT TGCTCTCCCT GCTCCCCCTCC CCCTTTGCA CCTTTCTTT TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCCTCAC CGCTTTCTCT CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTG CATTTCGGG TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTGCATT TTCGGGTGCT	1366 1416 1466 1516
40	CCTCCCTCCC CCTCCCCAGG CCTTTTTTT TTTTTTTTT TTTTTTTTT TTGGTTTTTC GAGACAGGGT TTCTCTTGT ATCCCTGGCT GTCCCTGGCAC TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG GCCTTCTTT TTTCTCTCT CTGGTCTCCC TAATCCCTT TCTGCATGTT AACTCCCCCTT TTGGCACCTT TCCTTACAG GACCCCTCC CCCTCCCTGT TTCCCTCCG GCACCCCTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC CCTCCCCCTC TTTGCTCGAC TTTAGCAGC CTTACCTCTC CCTGCTTTCT	1566 1616 1666 1716 1766 1816 1866 1916

5	GCCCCGTTCC CCTTTTTGT GCCTTCCTC CTGGCTCCCC TCCACCTTCC	1966
	AGCTCACCTT TTTGTTGTT TGGTTGTTG GTTGTGTTGTT TTGCTTTTTT	2016
	TTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC	2066
	CCTCTGTGTG CCTTTCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT	2116
	TCTGCCCTTC CTGTCCCTGC TCCCTCTCT GCTAACCTTT TAATGCCCTT	2166
10	CTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTGCTTCT GTGCACTTTT	2216
	CCTGACCTG CTCCCCCTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC	2266
	CCTTCTCCA GCCTGTCACC CCTCCTTCTC TCCCTCTGT TTCTCCCCT	2316
	TCCCTGTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCCTCC CTGCCCTGCTG	2366
	GACTTCTCT CCAGCCGCC AGTTCCCTGC AGTCCTGGAG TCTTCCCTGC	2416
15	CTCTCTGTCC ATCACCTCCC CCTAGTTCA CTTCCCTTTC ACTCTCCCT	2466
	ATGTGTCTCT CTTCCCTATCT ATCCCTTCC TTCTGTCCCC TCTCCTCTGT	2516
	CCATCACCTC TCTCCTCCCT TCCCTTCCCT CTCTCTTCCA TTTTCTTCCA	2566
	CCTGCTTCTT TACCCCTGCCT CTCCCATTCG CCTCTTACCT TTATGCCCAT	2616
	TCCATGTCCC CTCTCAATTCC CCTGTCCCAT TGTGCTCCCT CACATCTTCC	2666
20	ATTTCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC	2716
	TTCCCTTGC TTCTCCCTCC TCCCTTCCCC TTCCCTATG CCCTCTACTC	2766
	TACTTGATCT TCTCTCTCT CCACATACCC TTTTCTTCTT CCACCCCTGCC	2816
	CTTGTCCCC AGACCCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC	2866
	ATCAACAACA AGGAGGAAG AAACAGAGCA AAATCCAAA ATCAGCAGGA	2916
25	AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC	2966
	AAGTGGCTCC TATAACCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT	3016
	CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG	3066
	CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA	3116
	GAATCTGAAA ACTAGGGGCC AGTGGTTGT TTTGGGGACA AATTAGCACG	3166
30	TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA	3216
	TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTA	3266
	GGCTAAAGAT ACTTGGAACCC ATAGAAGCGT TGTAAAATA CTGCTTCTT	3316
	TTGCTAAAAT ATTCTTCTC ACATATTCA ATTCTCCAG	3355
	GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT	3396
35	AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT	3438
	ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA	3480
	AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA	3522
	GAG GAG GAG GAG GAG GAA ATG GGA AAC CCG GAT GGC	3564
	TTC TCA CCT TAG	3576
40	GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCTAACCA TATGCCGTGA	3626
	GCTAAAGAGCA TCTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA	3676

5	TCTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTAAGAA	3726
	CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTAGATT	3776
	GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA	3826
	GACCAAGTAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG	3876
	TTCTTATAGT ACCTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT	3926
10	TTCAAGAAAG ATCACACGCC ATGGTTACA TGCAAATTAT TATTTGTCG	3976
	TTCTGATTTC TTTCATTTCT AGACCTGTGG TTTAAAGAG ATGAAAATCT	4026
	CTTAAAATTT CCTTCATCTT TAATTTCTT TAACTTAGT TTTTTCACT	4076
	TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTA GATTCTTAA	4126
	AATGTTTTT AAAAAAAATG CAAATCTCAT TTTAAGAGA TGAAAGCAGA	4176
15	GTAACGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA	4226
	GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC	4276
	CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCAAATC	4326
	ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT	4376
	ATTTAGTTT CTCCCTGAGA AACAAATGACA AGACATAAAA TTGGCAAGAA	4426
20	AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTTTAT TTTCTTCTAC	4476
	AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT	4526
	TTTTTCCCC TTCATTAATT TTCTAGTTT TAGTAATCCA GAAAATTGAA	4576
	TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT	4626
	GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA	4676
25	AATAAAAGTT TGACTTGCAT AC	4698

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe

5 (2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

15	GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG	50
	GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC	100
	TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCCTGAG	150
	GGCCCCTGGA TTCCCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT	200
	TGGTCTGAGA CAGTATCCTC AGGTACACAGA GCAGAGGATG CACAGGGTGT	250
20	GCCAGCAGTG AATGTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
	CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT	350
	CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCCTGAGT ACCCTCTCAC	400
	TTCCCTCCTTC AGGTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC	450
	CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTG	500
25	TTAGAGTCTC CAAGGTTCAAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT	550
	CTCTCCCCAG GCCTGTGGGT CTTCATGCC CAGCTCTGC CCACACTCCT	600
	GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC	650
	ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACAAAGAGGC CCTGGGCCTG	700
	GTGTGTGTGC AGGCTGCCAC CTCCCTCTCC TCTCCTCTGG TCCTGGGCAC	750
30	CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC	800
	AGGGAGCCTC CGCCTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCCAA	850
	CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG	900
	TATCCTGGAG TCCTTGTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT	950
	TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG	1000
35	GCAGAAATGC TGGAGAGTGT CATAAAAAT TACAAGCACT GTTTCTGAA	1050
	GATCTTCGGC AAAGCCTCTG AGTCCTGCA GCTGGTCTT GGCATTGACG	1100
	TGAAGGAAGC AGACCCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA	1150
	GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC	1200
	AGGCTTCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCAGGCCATG	1250
40	CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT	1300
	GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA	1350

5	TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC	1400
	CGCACGCTAT GAGTTCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT	1450
	ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTT	1500
	TTCTTCCAT CCCTGCGTGA AGCAGCTTG AGAGAGGAGG AAGAGGGAGT	1550
	CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC	1600
10	ACCTCCAGG GCCGCCTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG	1650
	CCCATTCTC ACTCTGAAGA GAGCGGTCAAG TGTTCTCAGT AGTAGGTTTC	1700
	TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT	1750
	TCAAATGTTT TTTTTAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT	1800
	TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA	1850
15	GTCTTGTT TTATTCAAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG	1900
	ATAATAACAG CAGTCCAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA	1950
	AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC	2000
	CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG	2050
	GATTTCCCTG GCTTCTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG	2100
20	AATTCTTCCCT GTTCACTGGC TCTTTCTTC TCCATGCACT GAGCATCTGC	2150
	TTTTTGGAAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT	2200
	CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG	2250
	AGGTGGCAAG ATGCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA	2300
	GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCATGC CCTGAGCTGG	2350
25	GGCATTGGG GCTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	2400
	AATGATCTTG GGTGGATCC	2419

30 (2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

5	CCCGGGGCAC CACTGGCATC CCTCCCCTA CCACCCCCAA TCCCTCCCTT	50
	TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCCAGCC CAAGCCAGGC	100
	AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGGCC AGGTGCCAG	150
	ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTT	200
	CGGTCTGAGG GGCAGGCTTGA GATCGGTGGA GGGAAAGCGGG CCCAGCTCTG	250
10	TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCC	300
	AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT	350
	GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCCTTGCT GCTTAAACCA	400
	CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAAGG GCTGCTTAGG	450
	AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG	500
15	AGGGCTGAGG GTCCCTAAGA CCCCACCTCC GTGACCCAAC CCCCACCTCCA	550
	ATGCTCACTC CCGTGACCCA ACCCCCCTTT CATTGTCATT CCAACCCCCA	600
	CCCCACATCC CCCACCCCCAT CCCTCAACCC TGATGCCCAT CCGCCAGCC	650
	ATTCCACCCCT CACCCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC	700
	CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC	750
20	GCCACTGACT TGCAGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG	800
	AGGGACGGCG TAGAGTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG	850
	AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCCGCC ACTCCAAATA	900
	GAGAGCCCCA AATATTCCAG CCCCCGCCCT GCTGCCAGCC CTGGCCCCACC	950
	CGCGGGAAAGA CGTCTCAGCC TGGGCTGCC CCAGACCCCT GCTCCAAAAG	1000
25	CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC	1050
	TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA	1100
	GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCC CCAAGACTGC	1150
	ACTCCAATCC CCACTCCCAC CCCATTGCA TTCCCATTC CCACCCAACC	1200
	CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA	1250
30	CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC	1300
	TCACCCCTCAC TGCCCCAAC CCCACCCCTCA TCTCTCTCAT GTGCCCACT	1350
	CCCATCGCCT CCCCCATTCT GGCAGAAATCC GGTTTGCCCC TGCTCTCAAC	1400
	CCAGGGAAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC	1450
	AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG	1500
35	ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGGAGGCA AGGTGAGATG	1550
	CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCCAAATG	1600
	ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT	1650
	GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG	1700
	GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTCAAGGAGA	1750
40	GGCAGGGCCC AGGCATCAAG GTCCAGGCATC CGCCCGGCAT TAGGGTCAGG	1800
	ACCCCTGGGAG GGAAGTGAGG GTTCCCCACC CACACCTGTC TCCTCATCTC	1850

5	CACCGCCACC CCACTCACAT TCCCATAACCT ACCCCCTACC CCCAACCTCA TCTTGTCAAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAAGGG GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA GGGAGGCCTC AGAGGACCCA GCACCCCTAGG ACACCGCACC CCTGTCTGAG	1900 1950 2000 2050 2100
10	ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATT CCTGCATCTT	2150 2200 2250 2300
15	TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG CTGTCCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGGA TGGCGGTATG	2350 2400 2450 2500
20	TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGATTGGG GGTTGAGGAA GCACAGGCAC TGGCAGGAAT AAAGATGAGT GAGACAGACA	2550 2600 2650
25	AGGCTATTGG AATCCACACC CCAGAACAA AGGGGTCAAC CCTGGACACC TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA TCTGGGGCAG GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA GGGACCCCCA TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG	2700 2750 2800 2850
30	GAACATGAGG GAGGACTGAG GGTACCCAG GACCAGAAC CTGAGGGAGA CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCAGAG AGCATGGGCT GGGCCGTCTG CCGAGGTCTT TCCGTTATCC TGGGATCATT GATGTCAGGG ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAAG TAGAGGGAGC GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCAC	2900 2950 3000 3050 3100
35	CAGGACACAT TAATTCCAAT GAATTTGAT ATCTCTTGCT GCCCTCCCC AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCCTCCT GTCTTCCAT TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTTCAG ACCAGCAAAA GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCAGTGAGAA CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCAAC GAGTCCAGCC	3150 3200 3250 3300 3350
40	CACCCCTCTG GTAGCACTGA GAAGGCCAGGG CTGTGCTTGC GGTCTGCACC CTGAGGGCCC GTGGATTCTT CTTCTGGAG CTCCAGGAAC CAGGCAGTGA GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCC CTCACTTCTC CCTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG	3400 3450 3500 3550 3600 3650 3700

30

5	ATTCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC	3750
	CTTGTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC	3800
	TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCAGCT CCTGCCACAC	3850
	CTCCTGCCCTG CTGCCCTGAC GAGAGTCATC	3880
	ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA	3922
10	GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG	3964
	CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC	4006
	CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG	4048
	AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC	4090
	ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA	4132
15	GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC	4174
	CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT	4216
	CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA	4258
	GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT	4300
	CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC	4342
20	TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC	4384
	TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG	4426
	CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA	4468
	ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT	4510
	GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT	4552
25	GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG	4594
	CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC	4636
	AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG	4678
	GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA	4711
	AAGTCCTTGA GTATGTGATC AAGGTAGTG CAAGAGTTC	4750
30	GCTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG	4800
	GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC	4850
	AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCTGCC TCGTGTGACA	4900
	TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG	4950
	GTTCCTGTT TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTGGA	5000
35	ATTGTTAAA TGTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC	5050
	AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG	5100
	TAAGAGTCTT GTGTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA	5150
	TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG	5200
	CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCATT	5250
40	CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT	5300
	ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA	5350

SUBSTITUTE SHEET (RULE 26)

5	TAAAGAATTCTTCAGTGGCTCTTCTCTCCATGCACTGAGCA TCTGCTTTGGAAAGGCCCTGGGTTAGTAGTGAGAGATGCTAAGGTAAGCC	5400
	AGACTCATACTCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGT	5450
	AATCGAGGTG GCAAGATGTCCTCTAAAGATGTAGGGAAAAAGTGAGAGAGG	5500
	GGTGAGGGTG TGGGGCTCCGGTGAGAGTG GTGGAGTGTC AATGCCCTGA	5550
10	GCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCTTCTGGGGAGCTG ATTGTAATGATCTTGGGTGGATCC	5600
		5650
		5674

(2) INFORMATION FOR SEQUENCE ID NO: 9:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

25	CCCATCCAGATCCCCATCCGGGCAGAATCCGGTTCCACCC TTGCCGTGAA	50
	CCCAGGGAAAGTCACGGGCCCGGATGTGACGCCACTGACTTGCACATTGGA	100
	GGTCAGAGGACAGCGAGATTCTGCCCTGA GCAACGGCCTGACGTGGCG	150
	GAGGGAAAGCA GGCGCAGGCTCCGTGAGGAGGCAAGGTAAGACGCCGAGGG	200
30	AGGACTGAGGCAGGCCTCACCCAGACAGAGGGCCCCCAA TTAACTCCAGC GCTGCCTCTGCTGCCGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG	250
	GCTCAGTCGC CACCACCTCA CCCCAGCCACC CCCCAGCCGCTTTAACCGCAG	300
	GGAACTCTGGCGTAAGAGCTTGTGTGACCAGGGCAGGGCTGGTTAGAAG	350
	TGCTCAGGGCCAGACTCAGCCAGGAATCAAGTCAGGACCCAAAGAGGG	400
35	GACTGAGGGCAACCCACCCCCCTACCCCTCAC TACCAATCCCATCCCCAAC	450
	ACCAACCCCACCCCCATCCCTCAACACCAACCCACCCCCCAAACCCCAT	500
	TCCCATCTCC TCCCCCACCA CCATCCTGGCAGAATCCGGCTTGGCCCTG	550
	CAATCAACCCACGGAAGCTCCGGGAATGGC GGCCAAAGCACGCGATCCTG	600
	ACGTTCACATGTACGGCTAAGGGAGGGAAAGGGTTGGGTC TCGTGAGTAT	650
40	GGCTTTGGGATGCAGAGGAAGGGCCCAAGGCCCTCTGGAA GACAGTGGAG	700
	TCCTTAGGGGACCCAGCATGCCAGGACAGGGCCACTGTACCCCTGTC	750
		800

5	TCAAACTGAG CCACCTTTTC ATTCAGCCGA GGGAAATCCTA GGGATGCAGA CCCACCTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAA GGGGAGGAAG AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG GCTGGGGGAT CCTGGGCACA GTGGCCGAAT GTGCCCGTG CTCATTGCAC CTTCAGGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGGC TGGGACTTCA	850 900 950 1000 1050
10	GGTCAGCAGA GGGAGGAATC CCAGGATCTG CGGGACCCAA GGTGTGCC CTTCATGAGG ACTCCCCATA CCCCCGGCCC AGAAAGAAGG GATGCCACAG AGTCTGGAAG TAAATTGTTT TTAGCTCTGG GGGAACCTGA TCAGGGATGG CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCC CAGGGAGATA AGGTGTTGGT GTAAAGAGGA GCTGTCTGCT CATTTCAGGG	1100 1150 1200 1250 1300
15	GGTTCCCCCT TGAGAAAGGG CAGTCCCTGG CAGGAGTAAA GATGAGTAAC CCACAGGAGG CCATCATAAC GTTCACCTA GAACCAAAGG GGTCA GGACAAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTC CAGATCTCAG GGAGTTGATG ACCTTGTGTT CAGAAGGTGA CTCAGTCAAC ACAGGGGCCCT CTCTGGTCGA CAGATGCAGT GGTTCTAGGA TCTGCCAAGC	1350 1400 1450 1500 1550
20	ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCCT GGGCCAGAAT GCAGCAAGGG GGCCCCATAG AAATCTGCC TGCCCTGCG GTTACTTCAG AGACCCCTGGG CAGGGCTGTC AGCTGAAGTC CCTCCATTAT CTGGGATCTT TGATGTCAGG GAAGGGGAGG CCTTGGTCTG AAGGGGCTGG AGTCAGGTCA GTAGAGGGAG GGTCTCAGGC CCTGCCAGGA GTGGACGTGA GGACCAAGCG	1600 1650 1700 1750 1800
25	GACTCGTCAC CCAGGACACC TGGACTCCAA TGAATTGAC ATCTCTCGTT GTCTTCGCG GAGGACCTGG TCACGTATGG CCAGATGTGG GTCCCTCTA TCTCCTTCTG TACCATATCA GGGATGTGAG TTCTTGACAT GAGAGATTCT CAAGCCAGCA AAAGGGTGGG ATTAGGCCCT ACAAGGAGAA AGGTGAGGGC CCTGAGTGAG CACAGAGGGG ACCCTCCACC CAAGTAGAGT GGGGACCTCA	1850 1900 1950 2000 2050
30	CGGAGTCTGG CCAACCTGC TGAGACTTCT GGGAAATCCGT GGCTGTGCTT GCAGTCTGCA CACTGAAGGC CCGTGCATTG CTCTCCCAGG AATCAGGAGC TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTCA AGAGCAGAGG GGACGCAGAC AGTCCAAACA CTGAAGGTTT GCCTGGAATG CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCCTG	2100 2150 2200 2250 2300
35	GCCTCACCCCT CCCTATTCTC AGTCTGCAG CCTGAGCATG TGCTGGCCGG CTGTACCCCTG AGGTGCCCTC CCACTTCTC CTTCAGGTTC TGAGGGGGAC AGGCTGACAA GTAGGACCCG AGGCAGTGAG GGAGCATTGA AGGAGAAGAT CTGTAAGTAA GCCTTGTCA GAGCCTCCAA GGTCAGTTC AGTTCTCACC TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG	2350 2400 2450 2500 2550
40	CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAAG AGTCATC ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	2597 2639

5	GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	2681
	CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT	2723
	TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC	2765
	GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC	2807
	TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
10	GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
	CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG	2933
	ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	2975
	AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC	3017
	AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC	3059
15	TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA	3101
	GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG	3143
	GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
	CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	3227
	ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	3269
20	CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC	3311
	TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG	3353
	GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT	3395
	GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA	3437
	ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT	3479
25	GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT	3521
	TTG AGA GAG GGA GAA GAG TGA	3542
	GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	3592
	GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA	3642
	GGCCCATTCG TGCCCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG	3692
30	TTTCTGTTCT GTTGGATGAC TTTGAGATT ATCTTTCTT CCTGTTGGAA	3742
	TTGTTCAAAT GTTCTTTA ACAAAATGGTT GGATGAACTT CAGCATCCAA	3792
	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTATAT AGTTTAGGGG	3842
	TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTGTGAG	3892
	TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG	3942
35	AATTAGCACT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT	3992
	TGCCTTATAC CTCAGTCTAT TATGAAAAT TAAAAATATG TGTATGTTT	4042
	TGCTTCTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTCCTGT	4092
	TCACTGGCTC ATTTCTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
	CCTGGTAGTA GTGGG	4157

5 (2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

15

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGC	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
20 GGAAGCAGGC	GCAGGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCAGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
25 CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCCC	CAAACCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAACATCG	600
30 GAGCTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

40 (ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	GCCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGAAG GTTCTGAGGG	50
	GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
10	AGATCTGCCA GTGGGTCTCC ATTGCCAGC TCCTGCCAC ACTCCGCCT	150
	GTTGCCCTGA CCAGAGTCAT C	171
	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	213
	GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
	CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	297
15	TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	339
	GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
	CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
	GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
	CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
20	GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
	AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
	GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
	TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
	GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
25	GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
	CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
	AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
	CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
	TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
30	GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
	GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
	ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
	GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
	TTG AGA GAG GGG GAA GAG TGA	1116
35	GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
	GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCCTCC TGTGACGTGA	1216
	GGCCCATCTC TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
	TTTCTGTTCT GTTGGATGAC TTTGAGATT A TTCTTTGTT CCTGTTGGAG	1316
	TTGTTCAAAT GTTCTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
40	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTATAT AGTTAGGAG	1416
	TAAGAGTCTT GttTTTACT CAAATTgGGA AATCCATTCC ATTTGTGAA	1466

5	TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
	GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
	ATTCTTGCTT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
	ACCAGGATT CTTGACTTC TTT	1640

10

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-31 gene

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

	GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCAACCCT	50
	CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
25	GCCCCTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
	AGGACTTGGT CTGAGGCAGT GTCTCAGGT CACAGAGTAG AGGGGgCTCA	200
	GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
	CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
	TTCAGTCCTG CAGCCTCAGC ATGCCTGGC CGGATGTACC CTGAGGTGCC	350
30	CTCTCACTTC CTCCCTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGGACC	400
	AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG	450
	TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC	500
	TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCACAC	550
	CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
35	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	622
	GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG	664
	CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	706
	TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	748
	GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	790
40	CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	832
	GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	874

5 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943

10 2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

20

GGATCCAGGC CCTGCCTGGA	GAAATGTGAG	GGCCCTGAGT	GAACACAGTG	50
GGGATCATCC ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100
TCTTGATGGC ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCCTAAG	150
25 GCCCCATGGA TTCCCTCTCCT	AGGAGCTCCA	GGAACAAGGC	AGTGAGGCCT	200
TGGTCTGAGA CAGTGTCTC	AGGTTACAGA	GCAGAGGATG	CACAGGCTGT	250
GCCAGCAGTG AATGTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAAGACACAT AGGACTCCAA	AGAGTCTGGC	CTCACCTCCC	TACCATCAAT	350
CCTGCAGAAT CGACCTCTGC	TGGCCGGCTA	TACCCCTGAGG	TGCTCTCTCA	400
30 CTTCCCTCTT CAGGTTCTGA	GCAGACAGGC	CAACCGGAGA	CAGGATTCCC	450
TGGAGGCCAC AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTGT	500
TAGAGCCTCT AAGATTTGGT	TCTCAGCTGA	GGTCTCTCAC	ATGCTCCCTC	550
TCTCCGTAGG CCTGTGGTC	CCCATTGCC	AGCTTTGCC	TGCACTTTG	600
CCTGCTGCC	TGACCAAGGT	CATC		624
35 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA				666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA				708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC				750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT				792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT				834
40 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC				876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC				918

5	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044
	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
10	GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
15	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
20	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
	GCATGAGTTG CAGCCAGGGC TGTGGGAAAG GGGCAGGGCT GGGCCAGTGC	1628
	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGT A CATGAGGCC	1678
	CATTCTTCAC TCTGTTGAA GAAAATAGTC AGTGTCTTA GTAGTGGGTT	1728
	TCTATTTGT TGGATGACTT GGAGATTAT CTCTGTTCC TTTTACAATT	1778
25	GTTGAAATGT TCCTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
	AGTCTTGT TTATTCAAGA TTGGGAAATC CGTTCTATTT TGTGAATTG	1928
	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCAACGT	1978
	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA	2028
30	GTCTATTCTG TAAAATTAA AAATATATAT GCATACCTGG ATTCCTTGG	2078
	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTCTGTGA	2128
	ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAAGGCC	2178
	AGGATTAGTA GTGGAGATA TAGGGTAAGC CAGACACACA CCTACCGATA	2228
	GGGTATTAAG AGTCTAGGAG CGCGGTATA TAATTAAGGT GACAAGATGT	2278
35	CCTCTAACGAT GTAGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
	GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTG GGCTTGGGA	2378
	AACTGCATT TCTCTGAGG GATCTGATTG TAATGAAGCT TGGTGGGTCC	2428
	AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
	TCTGAGCAGT TCCTTGTA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
40	GGG	2531

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-41 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

20	GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
	GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
	TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCCTAAG	150
	GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
	TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
	GCCAGCAGTG AATGTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
25	CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
	CCTGCAGAAAT CGACCTCTGC TGGCCGGCTA TACCCCTGAGG TGCTCTCTCA	400
	CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
	TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
	TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
30	TCTCCGTAGG CCTGTGGGTC CCCATTGCC AGCTTTGCC TGCACTCTG	600
	CCTGCTGCCCG TGAGCAGAGT CATC	624
	ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
	GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG	708
	CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
35	TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
	GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
	GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
	AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
40	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044

40

5	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
	GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
10	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
15	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
	GCATGAGTTG CAGCCAGGGC TGTGGGAAAG GGGCAGGGCT GGGCCAGTGC	1628
	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGT A CATGAGGCC	1678
20	CATTCTTCAC TCTGTTGAA GAAAATAGTC AGTGTCTTA GTAGTGGTT	1728
	TCTATTTGT TGGATGACTT GGAGATTTAT CTCTGTTCC TTTTACAATT	1778
	GTTGAAATGT TCCTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT	1828
	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
	AGTCTTGT TTATTTCAGA TTGGGAAATC CGTTCTATT TGTGAATTG	1928
25	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTACCGT	1978
	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCTCA	2028
	GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTTGG	2078
	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTCTGT	2128
	ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAGGCC	2178
30	AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
	GGGTATTAAG AGTCTAGGAG CGCGGTCTATA TAATTAAGGT GACAAGATGT	2278
	CCTCTAAGAT GTAGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
	GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTG GGCTTGGGA	2378
	AACTCCATT TCTTCTGAGG GATCTGATTG TAATGAAGCT TGGTGGTCC	2428
35	AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
	TCTGAGCGGT TCCTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
	GGG	2531

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SUBSTITUTE SHEET (RULE 26)

5 (2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-4

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

15

G	GGG	CCA	AGC	ACC	TCG	CCT	GAC	GCA	GAG	TCC	TTG	TTC	CGA	40	
GAA	GCA	CTC	AGT	AAC	AAG	GTG	GAT	GAG	TTG	GCT	CAT	TTT	CTG	82	
CTC	CGC	AAG	TAT	CGA	GCC	AAG	GAG	CTG	GTC	ACA	AAG	GCA	GAA	124	
20	ATG	CTG	GAG	AGA	GTC	ATC	AAA	AAT	TAC	AAG	CGC	TGC	TTT	CCT	166
GTG	ATC	TTC	GGC	AAA	GCC	TCC	GAG	TCC	CTG	AAG	ATG	ATC	TTT	208	
GGC	ATT	GAC	GTG	AAG	GAA	GTG	GAC	CCC	GCC	AGC	AAC	ACC	TAC	250	
25	ACC	CTT	GTC	ACC	TGC	CTG	GGC	CTT	TCC	TAT	GAT	GGC	CTG	CTG	292
GGT	AAT	AAT	CAG	ATC	TTT	CCC	AAG	ACA	GGC	CTT	CTG	ATA	ATC	334	
30	GTC	CTG	GGC	ACA	ATT	GCA	ATG	GAG	GGC	GAC	AGC	GCC	TCT	GAG	376
GAG	GAA	ATC	TGG	GAG	GAG	CTG	GGT	GTG	ATG	GGG	GTG	TAT	GAT	418	
GGG	AGG	GAG	CAC	ACT	GTC	TAT	GGG	GAG	CCC	AGG	AAA	CTG	CTC	460	
ACC	CAA	GAT	TGG	GTG	CAG	GAA	AAC	TAC	CTG	GAG	TAC	CGG	CAG	502	
GTA	CCC	GGC	AGT	AAT	CCT	GCG	CGC	TAT	GAG	TTC	CTG	TGG	GGT	544	
CCA	AGG	GCT	CTG	GCT	GAA	ACC	AGC	TAT	GTG	AAA	GTC	CTG	GAG	586	
CAT	GTG	GTC	AGG	GTC	AAT	GCA	AGA	GTT	CGC	ATT	GCC	TAC	CCA	628	
TCC	CTG	CGT	GAA	GCA	GCT	TTG	TTA	GAG	GAG	GAA	GAG	GGA	GTC	670	
35	TGAGCATGAG	TTGCAGCCAG	GGCTGTGGGG	AAGGGGCAGG	GCTGGGCCAG									720	
TGCATCTAAC	AGCCCTGTGC	AGCAGCTTCC	CTTGCCTCGT	GTAACATGAG										770	
GCCCATTCTT	CACTCTGTTT	GAAGAAAATA	GTCAGTGTTC	TTAGTAGTGG										820	
GTTTCTATTT	TGTTGGATGA	CTTGGAGATT	TATCTCTGTT	TCCTTTACA										870	
ATTGTTGAAA	TGTTCCCTTT	AATGGATGGT	TGAATTAAC	TCAGCATCCA										920	
AGTTTATGAA	TCGTAGTTAA	CGTATATTGC	TGTTAATATA	GTTAGGAGT										970	
40	AAGAGTCTTG	TTTTTATTTC	AGATTGGGAA	ATCCGTTCTA	TTTTGTGAAT									1020	
TTGGGACATA	ATAACAGCAG	TGGAGTAAGT	ATTTAGAAGT	GTGAATT										1068	

5 (2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

15	GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG	50
	GGGACCATTG ACCCCAAGAG GGTGGAGACC TCACAGATTG CAGCCTACCC	100
	TCCCTGTTAGC ACTGGGGGCC TGAGGGCTGTG CTTGCAGTCT GCACCCCTGAG	150
	GGCCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT	200
20	TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC	250
	TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC	300
	GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG	350
	TCAGTCCTGC AGAACATCAGCC TCTGCTTGT TGTGTACCCCT GAGGTGCCCT	400
	CTCACTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAAG	450
25	GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	500
	ATCTGTAAGT AAGCCTTGT TAGAGCCTCC AAGGTTCACT TTTAGCTGA	550
	GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCC	600
	AGCTCCTGCC CACACTCCTG CCTGTTGCCG TGACCAAGAGT CGTC	644
	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	686
30	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG	728
	GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA	770
	TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA	812
	AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC	854
	CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG	896
35	TGG CTG ACT TGA	908
	TTCATTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA	958
	GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT	1008
	CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA	1058
	AGGAAGCGGA CCCCCACCAGC AACACCTACA CCCTTGTAC CTGCCTGGGA	1108
40	CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG	1158
	GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC	1208

5	CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG	1258
	GAGGGAGCAC AGTGTCTGTG GGGAGCCAG GAAGCTGCTC ACCCAAGATT	1308
	TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCAG CAGTGATCCC	1358
	ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA	1408
	CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATT CCTACCCATC	1458
10	CCTGCGTGAA GCAGCTTGAGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG	1508
	CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG	1558
	CTCCGTCCAG TAGTTTCCCC TGCCCTTAATG TGACATGAGG CCCATTCTTC	1608
	TCTCTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT	1658
	TGGATGACTT TGAGATTGT CTTTGTTC TTTTGGAAATT GTTCAAATGT	1708
15	TTCTTTAAT GGGTGGTTGA ATGAACCTCA GCATTCAAAT TTATGAATGA	1758
	CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT	1808
	TTTTTATTCA GATTGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT	1858
	TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAAC	1908
	TGATGACATA AAGAAATTAA AAGATATTAA ATTCTTGCTT ATACTCAGTC	1958
20	TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACTGGGA TTTCCCTGGC	2008
	TTCTTGAGA ATGTAAGACA AATTAAATCT GAATAAAATCA TTCTCCCTGT	2058
	TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC	2108
	CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA	2158
	CAGGGTAGTA AAGTCTAGGA GCAGCAGTCATAATTAAG GTGGAGAGAT	2208
25	GCCCTCTAAG ATGTAGAG	2226

(2) INFORMATION FOR SEQUENCE ID NO: 17:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-51 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

40

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG

50

5	GGGACCATT CACCAAGAG GGTGGAGACC TCACAGATT CAGCCTACCC	100
	TCCTGTTAGC ACTGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCCTGAG	150
	GGCCCATGCA TTCCCTTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT	200
	TGGTCTGAGG CCGTGCCCTC AGGTACAGA GCAGAGGAGA TGCAGACGTC	250
	TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC	300
10	GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG	350
	TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCCT GAGGTGCCCT	400
	CTCACTTTT CCTTCAGGTT CTCAGGGAC AGGCTGACCA GGATCACCAAG	450
	GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	500
	ATCTGTAAGT AAGCCTTGT TAGAGCCTCC AAGGTTCACT TTTAGCTGA	550
15	GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGTC TCCATTGCC	600
	AGCTCCTGCC CACACTCCTG CCTGTTGCCG TGACCAGAGT CGTC	644
	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	686
	GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC	728
	AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT	770
20	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG	812
	GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA	854
	TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA	896
	AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC	938
	CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG	980
25	TGG CTG ACT TGA	992
	TTCATTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA	1042
	GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT	1092
	CTTCGGCAAA GCCTCCGAGT CCTTGAGCT GGTCTTGGC ATTGACGTGA	1142
	AGGAAGCGGA CCCCACCCAGC AACACCTACA CCCTTGTAC CTGCCTGGGA	1192
30	CTCCTATGAT GGCGTGGTGG TTTAATCAGA TCATGCCAA GACGGGCCTC	1242
	CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA	1292
	GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG	1342
	AGCACAGTGT CTGTGGGAG CCCAGGAAGC TGCTCACCCA AGATTGGTG	1392
	CAGGAAAACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC	1442
35	TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTGAA AGTACTGGAG	1492
	CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCTTACCC CATCCCTGCA	1542
	TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG	1592
	CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT	1642
	CCAGTAGTTT CCCCTGCCCTT AATGTGACAT GAGGCCATT CTTCTCTTT	1692
40	TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG	1742
	ACTTTGAGAT TTGTCCTTGT TTCCCTTTGG AATTGTTCAA ATGTTCTTT	1792

5	TAATGGGTGG TTGAATGAAC TTCAGCATT CAAATTTATGA ATGACAGTAG	1842
	TCACACATAG TGCTGTTAT ATAGTTAGG AGTAAGAGTC TTGTTTTTA	1892
	TTCAGATTGG GAAATCCATT CCATTTGTG AATTGGGACA TAGTTACAGC	1942
	AGTCCAATAA GTATTCAATT AGAAATGTGA ATGAGCAGTA AAACTGATGA	1992
	GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATT	2042
10	GGTAAAATT TTTTTAAAAA ATGTGCATAC CTGGATTCC TTGGCTTCTT	2092
	TGAGAAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT	2142
	GGCTCATTAA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG	2192
	GTAAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG	2242
	TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT	2292
15	CTAAGATGTA GAG	2305

(2) INFORMATION FOR SEQUENCE ID NO: 18:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: cDNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-6 gene
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

30	TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
	CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
	GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
	GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
35	TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
	TGT GCC CCT GAG GAG	225

40	(2) INFORMATION FOR SEQUENCE ID NO: 19:
	(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1947 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
10 (ix) FEATURE:
(A) NAME/KEY: MAGE-7 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

15	TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA GAGCCCAGCC TCACCTTCCC TACTGTCACT CCTGCAGCCT CAGCCTCTGC TGGCCGGCTG TACCCCTGAGG TGCCCTCTCA CTTCCCTCCTT CAGGTTCTCA GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT	50 100 150 200 250
20	GGTCACAAA TGAGGCCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG GTTCCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG GATGCCCTGA GGCCCAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG GCTCCCGCCA CCGAGGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA	300 350 400 450 500
25	AGGCACCCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCAGT CCTCCCTGA GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGGAGGG GCCAACCAACC TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA	550 600 650 685
30	ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA CCT GCT TGG GCC TCT ACA ATG GCC TGC TGG GTG ATG ATC	727 769 811 853 895 937
35	AGA GCA TGC CCG AGA CCG GCC TTC TGA TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG GCAATCTGGG AAGCGTTGAG TGTAAATGGTG TATGATGGGA TGGAGCAGTT TCTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCGT GCTACCAGTT	964 1014 1064 1114 1164
40	CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTCCTA CCCATCCCTG	1214 1264

5	CATGAAGAGG CTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC	1314
	AGCCAGGGCC AGTGGGGCAG ATTGGGGAG GGCTGGCA GTGCACGTC	1364
	CACACATCCA CCACCTTCCC TGTCTGTTA CATGAGGCC ATTCTCACT	1414
	CTGTGTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG	1464
	GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCTGT TCTCTGGC	1514
10	GATTGGAGG TTTATCTTG TTTCTTTG CAGTCGTTCA AATGTTCCCT	1564
	TTAATGGATG GTGTAATGAA CTTAACATT CATTTCATGT ATGACAGTAG	1614
	GCAGACTTAC TGTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTAT	1664
	TTATGTAAGA AAATCTATGT TATTCTTGA ATTGGGACAA CATAACATAG	1714
	CAGAGGATTAGTACCTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG	1764
15	GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG	1814
	CCTGTAATCC CAGCACTTAA GGAGGCAGAG GCACGGGGAT CACGAGGTCA	1864
	GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA	1914
	AATAACAAAC TTAGCCGGGC GTGGTGGCGG GTG	1947

20

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-8 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

	GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTCAA	50
	TCACAGAGCA TAAGAGGCC AGGCAGTAGT AGCAGTCAGA CTGAGGTGGT	100
	GTTCCTCTG TATGTATACC AGAGGCCCT CTGGCATCAG AACAGCAGGA	150
35	ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG	200
	GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCTTCA	250
	GGTTCGAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCC CAGAGAAGCA	300
	CTGAAGAAGA CCTGTAAGTA GACCTTGTT AGGGCATCCA GGGTGTAGTA	350
	CCCAGCTGAG GCCTCTACA CGCTTCTCT CTCCCCAGGC CTGTGGGTCT	400
40	CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT	450
	C	451

5	ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA	493
	GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG	535
	CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC	577
	TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT	619
	GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT	661
10	TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT	703
	GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC	745
	CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT	787
	GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA	829
	TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG	871
15	AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC	913
	AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT	955
	GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC	997
	ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT	1039
	CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC	1081
20	ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC	1123
	TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA	1156
	TGGGAGGGAG CACAGTGTCT ATTGGAAAGCT CAGGAAGCTG CTCACCCAAG	1206
	AGTGGGGTGCAGGAGAACTAC CTGGAGTACC GCCAGGGGCC CGGCAGTGAT	1256
	CCTGTGCGCT ACGAGTTCCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG	1306
25	CTATGTAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA	1356
	TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT	1406
	TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG	1456
	GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTCCCT GCTCTGTTAC	1506
	ATGAGGCCCA TTCTTCACTC TGTGTTGAA GAGAGCAGTC ACAGTTCTCA	1556
30	GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC	1606
	AGTTCTGTT CTATTGGCG ATTTGGAGGT TTATCTTGT TTCTTTGG	1656
	AATTGTTCCA ATGTTCTTC TAATGGATGG TGTAAATGAAC TTCAACATTC	1706
	ATTTTATGTA TGACAGTAGA CAGACTTAAT GCTTTTATA TAGTTAGGA	1756
	GTAAGAGTCT TGCTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA	1806
35	ATTC	1810

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1412 base pairs
 (B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-9 gene
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG	TGTCCCTCAGG	TCGCAGAGCA	GAGGAGACCC	AGGCAGTGTC	50
AGCAGTGAAAG	GTGAAGTGT	CACCCCTGAAT	GTGCACCAAG	GGCCCCACCT	100
GCCCCAGCAC	ACATGGGACC	CCATAGCACC	TGGCCCCATT	CCCCCTACTG	150
15 TCACTCATAG	AGCCTTGATC	TCTGCAGGCT	AGCTGCACGC	TGAGTAGCCC	200
TCTCACTTCC	TCCCTCAGGT	TCTCGGGACA	GGCTTAACCAAG	GAGGACAGGA	250
GCCCCAAGAG	GCCCCAGAGC	AGCACTGACG	AAGACCTGTA	AGTCAGCCTT	300
TGTTAGAACC	TCCAAGGTT	GGTTCTCAGC	TGAAGTCTCT	CACACACTCC	350
CTCTCTCCCC	AGGCCTGTGG	GTCTCCATCG	CCCAGCTCCT	GCCCACGCTC	400
20 CTGACTGCTG	CCCTGACCAG	AGTCATC			427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA					469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA					511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT					553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT					595
25 CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC					637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC					679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT					721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG					763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG					805
30 GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA					847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC					889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG					931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC					973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC					1015
35 AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC					1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG					1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC					1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA					1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG					1225
40 CAC TAC GAG TTC CTG TGG GGT TCC AAG GGC CAC GCT GAA ACC					1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA					1309

50

5	AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG	1351
	GGA GAG GAG CAA GAG GGA GTC TGA	1375
	GCACCAAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA	1412

10 (2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-10 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

20

	ACCTGCTCCA GGACAAAGTG GACCCCCTG CATCAGCTCC ACCTACCCCTA	50
	CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT	100
	CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA	150
25	AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGGAGAAGA CCTGTAAGTT	200
	GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA	250
	CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATGCCCA AGTCCTGCC	300
	ACACTCCCAC CTGCTACCCCT GATCAGAGTC ATC	333
	ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA	375
30	GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA	417
	CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT	459
	TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC	501
	TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC	543
	CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC	585
35	CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT	627
	TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA	669
	AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT	711
	GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT	753
	TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG	795
40	ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT	837
	GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC	879

5 ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC 920

10 (2) INFORMATION FOR SEQUENCE ID NO: 23:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-11 gene

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

20	AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT	50
	CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT	100
	CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG	150
	GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAAG	200
25	AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG	250
	CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC	300
	AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC	350
	ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC	400
	TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC	450
30	TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG	500
	CCTGACCTGA TAGACCCTGA GTCCCTTCC CAAGATATAC TACATGACAA	550
	GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT	600
	GATCACAAAG GCAGAA	616
	ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT	658
35	GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT	700
	GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT	742
	GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG	784
	TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA	826
	GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA	868
40	GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT	910
	GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT	952

5	ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG	994
	GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT	1036
	CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG	1078
	TAC ATA GCC AAT GCC AAT GGG AGG GAT CC	1107

10

(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2150 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: smage-I

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	TCTGTCTGCA TATGCCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT	50
	CTCTACAGAC CTCTGTCCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC	100
25	ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC	150
	TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGCTCT	200
	GCCCTTGTAT GCAGGCCTAA GTTTTCTGT CTGCTTAACC CCTCCAAGTG	250
	AAGCTAGTGA AAGATCTAAC CCACTTTGG AAGTCTGAAA CTAGACTTT	300
	ATGCAGTGGC CTAACAAGTT TTAATTCTT CCACAGGGTT TGCAGAAAAG	350
30	AGCTTGATCC ACGAGTTCAAG AGTCCTGGT ATGTTCCCTAG AAAG	394
	ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT	436
	CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT	478
	TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT	520
	ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG	562
35	AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG	604
	GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT	646
	TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT	688
	TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA	730
	GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT	772
40	GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA	814
	GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG	856

5	AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG	898
	ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT	940
	AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA	982
	ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG	1024
	GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA	1066
10	CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG	1108
	TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC	1150
	TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA	1192
	TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG	1234
	ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG	1276
15	GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC	1318
	CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA	1360
	ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT	1402
	GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT	1444
	CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA	1486
20	GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT	1528
	AAC ATG TAG	1537
	TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG	1587
	AGAGTTCATA GCCTACCAAGA ACCAACATGC ATCCATTCTT GGCTGTTAT	1637
	ACATTAGTAG AATGGAGGCT ATTTTGTTA CTTTCAAAT GTTTGTTAA	1687
25	CTAAACAGTG CTTTTGCCA TGCTTCTGT TAACTGCATA AAGAGGTAAC	1737
	TGTCACTTGT CAGATTAGGA CTTGTTTGT TATTGCAAC AAACCTGGAAA	1787
	ACATTATTT GTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG	1837
	GATTGTCATG GCAATGTGAT ATCATAACAGT GGTGAAACAA CAGTGAAGTG	1887
	GGAAAGTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA	1937
30	TACTTTTTC TTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT	1987
	GACTTTACTC AAATTCACTA GAAAGTAAAT CGTAAACCTC TATTACTTTA	2037
	TTATTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA	2087
	GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA	2137
	GTTATCAGAG TCT	2150

35

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2099 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

5. (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: smage-II
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

10

	ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGT	AGCAGTCTCA	50
	AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
	TTTGCATGGG	CACAGGTTTC	TGCCCTGCA	TGGAGCTTAA	ATAGATCTT	150
15	CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
	TACAGGTCTC	TGCCCTTGT	TGCAGGCCTA	AGTTTTCTG	TCTGCTTAGC	250
	CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTG	GAAGTCTGAA	300
	ACTAGACTT	TATGCAGTGG	CCTAACAGT	TTTAATTCT	TCCACAGGGT	350
	TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCTA	400
20	GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
	AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
	TCTTTCAGA	TTCCTGTCTG	CCAGCTCTT	TACTTCAGCC	CTGAGCACAG	550
	TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGAAAACGA	600
	CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCCTG	CAGAGGAAGC	650
25	AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
	CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
	TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
	AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTCA	CACACACTGA	850
	AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
30	AAGTTTAAGA	TGAAAAGAAGC	AGTTACAAGG	AGTAAAATGC	TGGCAGTAGT	950
	TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
	CACGCCTAGA	ATTAGTCTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
	ACTCATTCCCT	ATTTGCTGGT	AGGCCTAACTG	GGTCTTTCCA	CTGAGGGAAAG	1100
	TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
35	TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
	CAATTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
	TGGCGAGCCT	GAGGAGTTA	TAAGAGATGT	AGTGCAGGGAA	AATTACCTGG	1300
	AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCCGTG	1350
	GGACCCAGAG	CCCATTGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTT	1400
40	AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAAGT	1450
	TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500

5	AAGGGTGTTC ATTCCAAGGC CCCATCCAA AAGTCCTCTA ACATGTAGTT	1550
	GAGTCTGTTC TGTTGTGTTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG	1600
	AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC	1650
	ATTAGTAGAA TGGAGGCTAT TTTGTTACT TTTCAAATGT TTGTTAACT	1700
	AAACAGTGCT TTTGCCATG CTTCTTGTAA ACTGCATAAA GAGGTAACG	1750
10	TCACTTGTCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC	1800
	ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA	1850
	TTGTCATGGC AATGTGATAT CATACTGTGG TGAAACAACA GTGAAGTGGG	1900
	AAAGTTTATA TTGTTAGTTT TGAAAATTAA ATGAGTGTGA TTGCTGTATA	1950
	CTTTTTCTT TTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA	2000
15	CTTTACTCAA ATTCAATTAGA AAGTAAATCA TAAACTCTA TTACTTTATT	2050
	ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG	2099

(2) INFORMATION FOR SEQUENCE ID NO: 26:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

30 Glu Ala Asp Pro Thr Gly His Ser Tyr

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(2) INFORMATION FOR SEQUENCE ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

40 Glu Val Val Pro Ile Ser His Leu Tyr

5

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5

(2) INFORMATION FOR SEQUENCE ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

10

Glu Val Val Arg Ile Gly His Leu Tyr

15

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(2) INFORMATION FOR SEQUENCE ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

25

Glu Val Asp Pro Ile Gly His Leu Tyr

5

30

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gly Val Asp Pro Ala Ser Asn Thr Tyr

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57

5 (2) INFORMATION FOR SEQUENCE ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Glu Val Asp Pro Thr Ser Asn Thr Tyr

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(2) INFORMATION FOR SEQUENCE ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

25 Glu Ala Asp Pro Thr Ser Asn Thr Tyr

5

30 (2) INFORMATION FOR SEQUENCE ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Glu Ala Asp Pro Thr Ser Asn Thr Tyr

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5 (2) INFORMATION FOR SEQUENCE ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Glu Val Asp Pro Ile Gly His Val Tyr

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(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acid residues

20 (B) TYPE: amino acid

(D) TOPOLOGY: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Tyr Met Asn Gly Thr Met Ser Gln Val

5

25

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 10 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

35

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu

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5 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met Leu Leu Ala Val Leu Tyr Cys Leu

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(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Leu Leu Ala Val Leu Tyr Cys Leu Leu

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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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Ser Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala

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5 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ser Glu Ile Trp Arg Asp Ile Asp Phe Ala

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(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Ser Glu Ile Trp Arg Asp Ile Asp Phe

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(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 16 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

35

Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Leu

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61

5 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu

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(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Ser Ala Tyr Gly Glu Pro Arg Lys Leu

25 5

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35

CGCCAATTAA GGGTCTCCGG TATCTCCCGC TGAGCTGCTC TGTTCCCGGC TTAGAGGACC 60

AGGAGAAGGG GGAGCTGGAG GCTGGAGCCT GTAACACCGT GGCTCGTCTC ACTCTGGATG 120

GTGGTGGCAA CAGAGATGGC AGCGCAGCTG GAGTGTAGG AGGGCGGCCT GAGCGGTAGG 180

40 AGTGGGGCTG GAGCAGTAAG ATGGCGGCCA GAGCGGTTTT TCTGGCATTG TCTGCCAGC 240

TGCTCCAAGC CAGGCTGATG AAGGAGGAGT CCCCTGTGGT GAGCTGGAGG TTGGAGCCTG 300

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5 AAGACGGCAC AGCTCTGTGC TTCATCTTCT GAGGTTGTGG CAGCCACGGT GATGGAGACG 360
GCAGCTCAAC AGGAGCAATA GGAGGAGATG GAGTTCACT GTGTCAAGCCA GGATGGTCTC 420
GATCTCCTGA CCTCGTGATC CGCCCGCCTT GGCCCTTCAA AGTGCCGAGA TTACAGCGAT 480
GTGCATTTG TAAGCACTT GGAGCCACTA TCAAATGCTG TGAAGAGAAA TGTACCCAGA 540
TGTATCATTA TCCTTGTGCT GCAGGAGCCG GCTCCTTCA GGATTCAGT CACATCTTCC 600
10 TGCTTTGTCC AGAACACATT GACCAAGCTC CTGAAAGATG TAAGTTACT ACCGATAGAC 660
TTTAAACTT CAACCAATGT ATTTACTGAA AATAACAAAT GTTGTAAATT CCCTGAGTGT 720
TATTCTACTT GTATTAAAAG GTAATAATAC ATAATCATTA AAATCTGAGG GATCATTGCC 780
AGAGATTGTT GGGGAGGGAA ATGTTATCAA CGGTTTCATT GAAATTAAT GTTATCAACG 840
GTTTCATTGA AATTAAATCC AAAAAGTTAT TTCCTCAGAA AAATCAAATA AAGTTGCAT 900
15 GTTTTTATT CTTAAAACAT TTTAAAAACC ACTGTAGAAT GATGTAAATA GGGACTGTGC 960
AGTATTTCTG ACATATACTA TAAAATTATT AAAAAGTCAA TCAGTATTCA ACATCTTTA 1020
CACTAAAAAG CC 1032

(2) INFORMATION FOR SEQ ID NO: 46:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

25 Met Ala Ala Arg Ala Val Phe Leu Ala Leu Ser Ala Gln Leu Leu Gln
5 10 15
Ala Arg Leu Met Lys Glu
20

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(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met Ala Ala Arg Ala Val Phe Leu Ala Leu Ser Ala Gln Leu Leu Gln
40 5 10 15

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5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Ala Ala Arg Ala Val Phe Leu Ala Leu

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(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

25	ATG CGA AGA GAA GAT GCT CAC TTC ATC TAT GGT TAC CCC AAG AAG GGG	48
	Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly	
	5 10 15	
30	GAC GGC CAC TCT TAC ACC ACG GCT GAA GAG GCC GCT GGG ATC GGC ATC	96
	His Gly His Ser Tyr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile	
	20 25 30	
35	CTG ACA GTG ATC CTG GGA GTC TTA CTG CTC ATC GGC TGT TGG TAT TGT	144
	Leu Thr Val Ile Leu Gly Val Leu Leu Ile Gly Cys Trp Tyr Cys	
	35 40 45	
40	AGA AGA CGA AAT GGA TAC AGA GCC TTG ATG GAT AAA AGT CTT CAT GTT	192
	Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val	
	50 55 60	
	GGC ACT CAA TGT GCC TTA ACA AGA AGA TGC CCA CAA GAA GGG TTT GAT	240

64

5	Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp				
	65	70	75	80	
	CAT CGG GAC AGC AAA GTG TCT CTT CAA GAG AAA AAC TGT GAA CCT GTG				288
	His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val				
10		85	90	95	
	GTT CCC AAT GCT CCA CCT GCT TAT GAG AAA CTC TCT GCA GAA CAG TCA				336
	Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser				
	100	105	110		
15	CCA CCA CCT TAT TCA CCT				354
	Pro Pro Pro Tyr Ser Pro				
	115				
20	(2) INFORMATION FOR SEQ ID NO: 50:				
	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 676 base pairs				
	(B) TYPE: nucleic acid				
25	(C) STRANDEDNESS: single				
	(D) TOPOLOGY: linear				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:				
	TCTTCATACA CGCGGCCAGC CAGCAGACAG AGGACTCTCA TTAAGGAAGG TGTCTGTGC				60
30	CCTGACCTCA CAAGATGCCA AGAGAAGATG CTCACCTCAT CTATGGTTAC CCCAAGAAGG				120
	GGCACGGCCA CTCTTACACC ACGGCTGAAC AGGCCGCTGG GATGGGCATC CTGACAGTGA				180
	TCCTGGGAGT CTTACTGCTC ATCGGCTGTT GGTATTGTAG AAGACGAAAT GGATACAGAG				240
35	CCTTGATGGA TAAAAGTCTT CATGTTGGCA CTCATGTGC CTTAACAAAGA AGATGCCAC				300
	AAGAAGGGTT TGATCATCGG GACAGCAAAG TGTCTCTCA AGAGAAAAAC TGTGAAACCTG				360
	TGGTTCCCAA TGCTGCAGGT GCTTATGAGA AACTCTCTGC AGAACAGTCA GGACCACCTT				420
	ATTCACCTTA AGAGCCAGCG AGACACCTGA GACATGGCTG AAATTATTTC TCTCACACTT				480
	TTGCTTGAAT TTAATACAGA CATCTAATGT TCTCCTTGG AATCCTGTAG GAAAAATGCA				540
	AGCCATCTCT AATAATAAGT CAGTGTAAA ATTTTAGTAG GTCCGCTAGC AGTACTAATC				600
	ATGTGAGGAA ATGATGAGAA ATATTAATT GGGAAAATC CATCAATAAA TGTTGCAAAT				660
40	GCATAGTAAA AAAAAA				66

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13585 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: at positions 9421-9456, the "Ns" refer to an unsequenced portion of from 4.7 to 5.3 kilobases

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

20	CCGTCAGAAA TCTAAACCCG TGACTATCAT GGGACTCAAA ACCAGCCAA AAAATAAGTC	60
	AAAACGATTA AGAGCCAGAG AAGCAGTCTT CATAACCGCG GCCAGCCAGC AGACAGAGGA	120
	CTCTCATTAA GGAAGGTAAG AGCGTGCCT TCTGCCATA ATCATAGTCC TCTTCTCCCA	180
	GAATAGGATT TGGGAAATTG TGGCTAAGTC CTCTGCCTAC CCTCATTGCC CCGCTGATGT	240
	GTGACATCAA CAGAATTCTT CCGCAACGTT TGTCAGTCTC CAACCTCAGA GGGCTCACAA	300
25	AGCCTCCTCC TGAATCCTCT CTCAGTCCTC CAACACTACC AAGAAGAAAA GCAATTATTC	360
	AGGATGGCAT CTTGCTGGGG AGAAGCAGCC TCCCTGAGGT AGATGTGTT TCCTGTCACT	420
	TAAAGAACCA CTTCTCCTGG TCTGAGTAGT AAGAGGGCGA TTTGCTGTTG CTGCACCATT	480
	TGCCAAGGCT CTGAGTTTGA GGTATGGGAT GTATTAAAAC AATTAAATGA AGAATTAAGA	540
	TTCCATTCTG TCATTTGAA CACAGGGTTC AGTCCTATAT TATTCACTTG AGAGGACTGG	600
30	TGAGTTTGAC TTTCATTTCT TTTTTACAAC TGGGAAGGGC AAATTACACA TAAAATGTCC	660
	CAGTGGAAAG GGGTCATGTG TCGAAATCCC CACTCTTCTG TCTCACCTCT CCCTGTTGTT	720
	TTAAACTGGG GCTCATTAAT ATAATTCTAT GGGGATCACA CCTTGAATAT TCATGAGGAC	780
	AGTAAGAGAG CAGAAAATA CACAATAATA AGGAAAGGAG CTTCCATTAT TGGTTTTAA	840
	TGAGCGTACT TGAATTACGG CCACTGCAGT TTATGGATAT TTTTGTTGT TCATTTGTAT	900
35	GTGTTATAGT TAGAAAAAAA AAGAATCCTA GCCAAGGGAC TTGAACCAGA GAGAACAGA	960
	AATTGACTTA AGTAGGAAGG GAAACACATT ATTAGATAAA GTCAGGTCTT GGGCTTCCTC	1020
	GGCTGTTT GGGTGGAGTG CCTGGGGACA GGCTGAAGCC CCTGTGTGGG GTGGTTTCCT	1080
	TTGCTGAAAA GCTGGGCTGG AAGATGTTGT GCTCAGTGCT CAACCTCATG CACCCCTCGCG	1140
	AGGCACAGGC AACGGGTGCT CTGGGAAACA CACGTTATGT ATCATAGCCT CTGTTTGCT	1200
40	GTGGGATTGA TATCCAATAA TAACTTGGA GAAAAATAAC TCCTCTTATT TTGTTAGCCA	1260
	CAGCCCTGGG CCAGGGAAAGG TGGAGAATCA GTGAAAATGC ATTTGTTTG TTTCTCTAGA	1320

5	AGTTTATGGT GCAGAGTCAA ATTGAAGGCA AATGAGGAAT ATTTTTCAT TAAATAATAA CTCAACTTGC AAGTCTTT TGCTTTGTT TGTAGTTCT TCTTTGAACt TAATTTCAAG TTAGTAGGAG GGGTTAGAAA CCTGAGCTAT TGCTAAAGCC CTTGATATGA ATGAAAGAAG CAGGTGCAAA TCCCCTACA GAGAGAAACC AAAGGGTCCT GGCTATGGAT ATTGGTCACC TAGTCAGGAT GCTGTTGTGG GTCTTATGA GATGATGAAT AGGGTGGCTT TGGATGCATT	1380 1440 1500 1560 1620
10	AATGATATT ACATGCTCCT TCTGTTAGTG TCCTGTGCC C TGACCCCTACA AGATGCCAAG AGAAGATGCT CACTTCATCT ATGGTTACCC CAAGAAGGGG CACGGCCACT CTTACACCAC GGCTGAAGAG TAAGTTCAAA ACCAGACCCA GCAGGGCTTC CAGTTGCCG TTTGCTGACA CAGCCTGCTG ACTTCCACCA GTACATGCCT GTCGTAAT CTCCCTAGTG TTTATCTCCC CAGACAGTAA CATCCCTGGC AACAAAGGGG A GGAGATTCTG TGCTTCTATA AGGGGCTCAG	1680 1740 1800 1860 1920
15	TCAAGCTTCT CTGAGGCCAA ACAGGCAGGA AGATGGGAAT GGTATAAGGT TGGATCTTGC CATTTTGGG TGCACTTTG ACTATTGGGT CTTATCTGTA GGTTCCCAAG TGGAAAAAACAA TCTGTTCAGG ATCACAATGC CTCTCTCCTC AATCCTGTT CTGTCCTC CACTCAAATT CCTGAAGGTG GTTGAGAC AGAATAAAAG TGAGTTGCCA AGGAGCCAGT AAGGATGACG GGCAGGTGTG TGTGACTCAG CCCACAGCCA GACTCGAGAG GAAGATGGAG GTCACAGCCT	1980 2040 2100 2160 2220
20	TTGCACTATA ACTTTATCCT AAGGAAAGAC ATTGGGTTTT ATGAGTGAAT TAAAAATAAG TATTATATG ATTAAGCATT TCTAAATGCT AAGCATTGTA TACTGGCGTG AGACACTGTT TTTATCTTG AAAAAACTCA CAACTTAGTG GGAGAGTTAG GCATGAGATT AATTTCAGCA AATGTAAGTG CGGTAATGAA AACCCAGAGG CTGCAGGGAC ATACTCTGTA TGTGCTGGGA GTGGGAAAGG GACACTACT GTACGTGCTG GGTGGCAGGG GCAGGGGAGG CCCCACCCCTC	2280 2340 2400 2460 2520
25	TGCGTGGGAC TGTAACAGGA CAACACCCCTC TTATGTGGTC TGTCCAGAAC TCCCTGTGAA CCTGCTCTT CTTGGAAAG AGCTGTTGAA CAATCTTGTA TAACAGTCAA CCGCAGGACC AGCAAGATGT AAAGCCAAC AAAGGCACGT AGGAAGAGTT CAGGAAGACA GCATTTCTC AGAAGACCCCT GGTATAGGAT CCTCTAATAT CCCTGGCCAA TTGGAGATGA GGGCGGCGGT ATCCTCTCAG AAAATGTCTC GACAGCAAA ACACTCTT TGAGGGAGGG GAGCCCATTG	2580 2640 2700 2760 2820
30	CCCGTGCTAT TAGTTAGGGT ATCGTTTCAG CTTGTGTATA ATCACTCAAC AGACTCTTAA AAATATACTT TTATGTCTCG TGAAAAAATT CAAGAGTAAA GAGTTCAAGG CCTGTTCGTT TTCTCTTGC TGGTTACTCC CTTGGGATCG TCACCTTGTT CCCCATGGCT GAAGATGTTG TGCCTACACC TCCACATCTT GCCAACAGAA AGCAGGAGGT GAAGGAGAGG CTAGGACCAT TCCCTTCAAG GGGCACACGT CACTCTGCT TATTGCTCCA CCCCCGCCCC CCGCCCCGTG	2880 2940 3000 3060 3120
35	GCACCCACCC TGGTGGTATC ATTCTGCTG TGGTGTAAAT GAAGAAAGGT TTAGAGAAAT TAGGAAATGT GTGGCCAGAC ATGGTGGCGC TGGGATTAA ATCCAGGTCT GTTGCCTCC AGAGTCCATG CTCTTAAGTG TTATGCTGCA GGCCAGCAGA GGCAAATATT TGCACAATCC CATCCGACGA GAGGCTAGGG CAGAGGTCAAG TATCTCTCAG TGTGAAGCTG GAGGCTGATG	3180 3240 3300 3360
40	CTAGTCAGCT CAGTAGGCCG AAAGTGGAGT TGTCTTTGC CATGTAGGGC CATCATGCC AGCTGGGAA CCTCATAGCC AGGTGTACCC ACAACCTGAA CAAGGTAACt TTCAGGGTCT AGTCAGGAAG AAACCAACTA GATGGTCAA CATAGAGACT TTAATATAAG AAGCTGGTTA	3420 3480 3540

5	AACAGGCATG GGACTGAGAC TGAGGAGGCA AAGAAGGCAT CGGGGCAACC AAGGCTGTAC CCACAGAATG CTGCTTCTAC CCCC GTGTCT GGGGTAACAA ACGGAAGGGT GAGGCCATCA GGACCTAGAG TTGGGAGGAG GGACGCCACA GAAATGGGAC CCAGATCTCT AAGGAGAGAT TTTGTTTGG CTGGTTCTGG TGTCTCAAGA GCTTAGAAGT GAGGGCATG AATCAAATAC TCAGGCCTCT GAGGTCA GCC AGTGCTCTGC TGGGGAGGGG CATAATGAAG CTGGCTCTGA	3600 3660 3720 3780 3840
10	CAATGCCGGA AAACGAGCTG GTGCTGGCA TATACAGACA ATGTGAGCAT TGCTGGGGTG ATCCTGACAG GAGCCAGAAG CACACTGGAA GGAGCTGCTC CTTCTTGATG CCCCAGGTTT GTAGGCACCC TCTAGAGTAC TCTAATGGGA GCCAGTGGGC AAAGGAGAAG TGGCATTG AGAGTCCAGT CCCAGCATCA CAGAGCAGAG CATA GAAAGG TAGGTTTGGA GAAGAGGGAC AATGGCTAA TAAAGGGCAA AGGGGGTTAT GACCACTATC ATGTGAAGGA ACCCCTTGAC	3900 3960 4020 4080 4140
15	TGAAGGCACA AGCTTTCTGT GTCTTGCAAC CTGAATGACG TGCA TAAAGCA GGGTCAGGTG GGTTATCTGA CATTTCCTT GAGAACAAAGA GGGAGCCTCT GGATTCAGC ACAAAAGAAA AATAACCACT CAACCCGTAT GCGTGGGAGC TATCCTTAA AGAGAAAGTA ATTCTTTTG ACATTTGCT GTCTGTAGAA GGGTCAGATG GCCAAAGCTT CCAGCACAAT GAAACACTTA ACTTCAGTCT GTGAGTGTAG GAACCCCTGA ATACATGGAA CATCATCATC TTGTGCAGGT	4200 4260 4320 4380 4440
20	ACTGAAGGAG ATCGGTCCAG AAAATAAGTA ACTGCACATG GCCACCAATG TCAAAAGTCA TTCCTCTCAT GAAAAGTCCC TGCCCCATT GCTGTTGTT TAAATAGGTG GGATGGAGGT AGGGGAATGG GGCCATCTTC TTTTTTTTT TTTAATTTTT TTGCATAAAA TCCAGATCCT GCACAATGGG GCAATCTCA TTAAAACAAT GCATCCCTAA GATCTGAGAA TATTTATCCT TCTCACAATT GTGCCAGCAG GTGGAAATGAA GAAGAATGAT GCAAAATAAG TTCCCACATC	4500 4560 4620 4680 4740
25	CAGCCAAGAA GGACTACATA CCTGCTTGG GTATTATGTA TCCCTTGAA ACCTCAGTGG AGAGCAGTTC TCACAGTTGG GTGGACACAA GTCATCCATG GAACTTGTAA AAATGCAGAT TTCTAGGTGC TGCCACCTAA GAGGCTGATT GGGTAGGCCA GGGGTGGAGT CCTATGATCT GCACCTTAAC GTGCATCTCA GGTGATTCTG CTGCAGGTGG TATTTGAAG ACACTCTGAG GCGCCCTGCC AAGCTGGCA GTGGGTTCTT CCAATGTGTC AGGCATAACCC TGGTGCTTT	4800 4860 4920 4980 5040
30	CGCTCTCAGT CACTTGGGCA TGTTGTGAGT ACCACGTGAC CATGCATAAA GTGCTGTAAC AGAGCTCTGT CTGTGTCAAG ATATTCAAGT GGACGCCACA GGGTAAAATG AGAGCACAGG CATGTTGGGA GTTGAATCAG CTGCCTTCAG TCACGAGAAC ACAC TGAACA CTCCTTGTA CAGCTTCAGT TCAGGAAAGA GTGACTCTGC AGGAAAAGCA CTGGCCTGGG AGACCTGGAT CTGGCCCAA TTCTGGTGCT CACTTGCTTG GTCTCCGTT CCAGTTGCTG TGAATGTTGG	5100 5160 5220 5280 5340
35	TTCTGCCACT TGCTGGTTGT GCAGCCCTGG GCACCTGACC AGCATAATGT CAGCTGAAA ATGAACATCA TTCTTAACTC CGAGGACTGT GGTAGGATG AAATAAAAGC ATATATGTTGG GGGTGCCTAG CCCAGTGCCT GGCACAAATT GGTGCTCAAT GAATGGTAGT CACTATGGTT ATGGTAATGT TGATGAATCT TCATAGGTCT CAGCTTCTG ATCTATAAG CGGGTGGACT GACCTACATA AGTCAGAGTT TCCATCTAGC ACTGTCA TCC CAGCCTT GAGACAGAAG TTGTCCAGTA	5400 5460 5520 5580 5640 5700

5	GATGGTACTG AGCAAAAGTC TCTCCAGCAG AAGCCTTAGT TAAACCTTGC TTCTCCTGTA	5760
	GCTGCTAGT CTCTGTAAG TCACTCAGCT CTGCAGAAAC TTTCTTAGCG AGTTGACAAC	5820
	CACAGATAAC AGAGTCAGTT CTGTCGATT TGATCATGCT GTGATCAGGC AGATGTTAGC	5880
	TAATTGATGA TGCTTGCCCC GAGTGAACAG CTCCAGGCC CGTGTAGGAGG GTCTTGTGG	5940
	TAACTTGTG GTAACTGTAA TGCTTCCCAG GGGTCACTGA ACACAGGGCC CAAGAGGCTG	6000
10	GTGTAGACCC CCAGATTGGC ACCCTGCTGC TTAGACAAGA TCCTTCTCAA TAAGTAATGC	6060
	CATAGCTTG CTGTAGGTTG AGCCCAGACA CTTCTCCCTA GGGCTGCAAG GAGCAAAGCG	6120
	GGGAGTTAG GGAAGGGAGG GCACGAACAT AATTGAGACG GATTCAAGGTT CAAATCCAGC	6180
	CTCTGTTTG TGCTAGCTCT GTATGATCAC CAGCGAGTCA TGTATCCTCT GCCTTTATT	6240
	TCCTCTCTG TGAAAATAGG GGATGATAAA TTGTGTCTAC CCTCCAGTGT TGATGTGAGA	6300
15	ATTGAATAAG CTAATGAATG TTTAGCACAG CACCTGGCTT TTAGTAGATG AGTCAGTGT	6360
	AATTCTATT TTCTCTTGT GGGCTGAGTT GGAGAAAATG TTTAAAACA GCCTGATGAG	6420
	AAGAAAAGAT AATTAGCCC CAATAAAATAC ATTGTCCACA TAAAGACAGT TACTATGGCA	6480
	CTTCTCATAC CTGGAACCTTG GGTGCCTGGG CCATGCAATT AGCAGAGTTC CTGTGGGCAC	6540
	ACACTTGAGA GGCTCCTAAA GACCTGGGTT AGATCCAGGT GCTGGAGGCC TGGTGGGTG	6600
20	CCAGTGTGGG AGGTGGAAA CTACTTGGAC ACTGGGAGAT GCTGCTCTGG GTGTCAAAG	6660
	TCCATATGAA GAGGAAGACT GATTTATGCT TCATCATAAT GTAGAACAAAT GTTCAATGA	6720
	CAAAGTGGAT TTGTCTATCT CTTGGGCCAG GCCGCTGGGA TCGGCATCCT GACAGTGATC	6780
	CTGGGAGTCT TACTGCTCAT CGGCTGTTGG TATTGTAGAA GACGAAATGG ATACAGAGCC	6840
	TTGATGGTTG GTAAAGTTCC CACTGCTGAA ATCCCTCAA GTCCAGGGCC CTCTTCCAG	6900
25	TTCTTCCTC TGAATCTCTG GAGAGTCAGA TAATTGCCTC ATTATAACCT TCAGCTCTGA	6960
	TTCCGGCTTC TGATGCCCT TTTGCTACAT TGTACTTTGG CAACTCTACC TTTGCCTCTG	7020
	CTCAGGCATG AACCTCAACC AGGAACCTGC CCTGTGTCTT AGTCTGTGAT TATAACATAA	7080
	TACGAGAGAC TGTAATTAT AAATAAAATGA AATTCTTTG GTTACAGTT GGGAGGCTGG	7140
	GAACTCCAAG ATCTAGGGGC CACACCTGGT GAGGACTTCT TGCTGTGTCA TATCATAGTG	7200
30	GAAGGCATCA CATGGGCAAG GGAGTGAGAG AGCAAGAGGG AGCTGAACTC ATTNTTTTTT	7260
	TTTCTGAAA CAGGAAATCC TGGGATGGAG CGCAGTGGTG ATCATGAGTC ACTGTAGCCT	7320
	TGACCTCCTG GGCTCAAGCC ATCCTCCTGT CTCAGCCTCC AGAGTAGCTG GGACCACAGG	7380
	CACGTGCCAC CACACGGCT AATTAAAAAA AAACCTTTTT TTGTAGAGAC GAGGTCCCAC	7440
	TATGTTGCCCT TAGGCTGGTC TCAAACCTCT GGGCTAAAGT GATCCTGCCT CGGCCTCCCA	7500
35	AAGTGTGGG ACTACAAGTG TGAAACACTC CACATATGGC CCAAACACTCAC TTTTATAACC	7560
	AACCTACTTT TGCAATAACA AACACACTCC TGCAATAACA CAATTAATCC ATTGATGAG	7620
	GACAGAGCCC TTGTAACTTA ATCGACCTCT TAAAAGTCCT GCCTGTTACC ATTGTTGCAT	7680
	TGGGGATTAG GTTCCAATA CACGAATTTT GGGGGACACA TTCAAACATAGCACCTGT	7740
	TCTTTGGTTC TACTCATAGC AGACTTGGGT ACCTGGATGT TGTGTGTAGC TAAGCACTGA	7800
40	CGGTTTATAG GGCACAGGGG AAGGGGTTTG AGGTTCCCTT ATAGCAAACA GGAGTATATT	7860
	AGACACCTCA GGTTTACCA CTTCTGGAA TTCTGCTGG TTCTGTTACT CCACTTTGTG	7920

3	ACCTGCTCTT CCTACTTTTC TTCTTCACCC CTTTCCTCAC TGTTTACCTG TGAATTCCAA	7980
	GTTCTTCTGA CTCTACACTA AGCATCCAG GATATCATCA GTGCGATGAG GAAACCATCC	8040
	TCCTGCATC AGCACAAAGG GTCACTTGTG TGTTTTTAA CAGGCTGCAT CCTTCTTAGA	8100
	TGGCCAAAGG TTTAATAGT ATTTTTTCT TCTTTACCCA AATATGCAGG AAGCTAACAC	8160
	AATTACACAA TCCAATCTTC TGGTACCAAGT ATCCTCCATG AATGGGAAAC ATCAACTGAG	8220
	TTTATAAGCT ATAAAAAATTA CAGGTTTCAG CAATCTTGCT TAAAGCCAGG TAGCACTTCA	8280
	GCACCTTCAGC ACCCGAAGCA TTCTCCATAG ATCTCGCTGT CTCTCTTCT TGTTATTACA	8340
	GATCTGAAAG CTTTCAGGT TGATGCATAA TGGA _n GTATCTTCC AAAAGATGTT	8400
	GGAAAGTCCC ATTCTCATTG AGCAAGCACT TCATTTAGAG GAAAAGGTCC TGTGAAAGAG	8460
	AGGAGGGTTG GTGTGGGGTG GGGATTGAAG CTTGGCAAGC TGATAAGGAG AAGGTGAGAG	8520
5	ATACAACCTCT GGATTCTTTC CCTCTTGCC AAGAAACTTG GGCAGTCTCA TGTCTCATGT	8580
	CTCCTGTTCC CCAATGTCTT TCCAGAGCAT AAATACAAAT ACAAAACCATC AAAGGCAAGT	8640
	CAAGTCTGGG GGCTGACACA CCCACCGAGC ATAGCCCTCT AGTGTGCTGA CATCTAGTGG	8700
	GAAGGAGGAG GAGTTGATGA ATCTGAACAA GACTCCAATA TTGGAGGAAA TACTTGAGGA	8760
	AAGCCTTGGG TTAGAAAGTT AGGGATAGAA TTCTGCTCA TACGGCTGTC CACAACAGGT	8820
0	TAGTAGGGGA GGACTTTAAT CTCTGCCATA GAACTCCATT TGTAACCTCA GCATGGGGTT	8880
	ATGACATTGC CTTGTAATTG GCTATTTACT TTTTGCCTCT TCGACCCCTC CGCTTCC	8940
	TATGTATGAA CCACAACAGA GAATATTTCT AACTCATCTT CATATCTCA GTGCCTAGCA	9000
	CAGTGCCTGG TACATGGTAG TCACTCAATT GTGTTGCATT AGGACTTGGT CCCATTGTCT	9060
	GCCATTGAGT TGCTGGAGA CTAGAATTCA ACTTCTCCAA GATTCACTAG CTCTATTTA	9120
15	CACCCAGACA TGTTGAAAT CTGTGATGTA ACACAATGTA TATCCATT TATTTAATAC	9180
	ATATTTCTT CTATATTTG ATTCATTAT ATATTTGTAT ATCAAAAACA AAATGTTAG	9240
	TCTTCAAGA AGTAAAGCTA TACAAACTCA ATATGTTGGT ACTCATTCC TAACATATAAT	9300
	TATTAGTTTG ATCCTATTGA ACACAAATGC AGTAATTTT CTTTCTGCT TCAATGCTCT	9360
	CATCTAAAT TCATTTAATT GAAAATAAC AGAGAGTCTT AATGTCTGT GCTCAGACAC	9420
20	TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNGAGT GCAGTGGTAT GATCTGGGCT	9480
	CACTGCAAGC TCTGCCTCCT GGGTTCATGC CATTCTCCTG ACTCAGCCTC CCAAGTAGCT	9540
	GGGACTACAG GTGCCGCTA CCATGCCTGG CTAATTTTT GTATTATAG TAGAGATGTC	9600
	ATTCACTGT GTTAGGCCAGG ATGGTCTCAA TCTCCTGACC TCGTGATCCA CACGCCTTGA	9660
	CCTCCCAAAG TGCTGCGATT ACAGGTGTGA GCCACCGTGC CCGGCCTTAT ACTTCTTTT	9720
25	TACTTTTTT CAGTGGTTTC CCTAGAGTTT GCAACATACA TTTACAACTA ATTCAAATCC	9780
	ACTTCAAAT AACACTATAC CATTCTCATAG GCATTATGAG TATCTAAAA TAATCCTAAT	9840
	TCCTTCTCC TGTAACCTAA AAACAAAATC CAAATCCTC CAAACAACTG AATGGACCC	9900
	CTCTTCACCA AGGGGACCCC AGGGAAACCT GAAAACGTGA GTGTTGCCA TGACGGGAAG	9960
	GGAGGTGAGA GATGCTCATT ATACTCCCTC CCTTTAGAG TTTAGGTAC AACTGACCAG	10020

5	CATTAATTT AAAATAGAGA TTACAGGACT GACAGAATGA ACTCTTGTC GCAATATCAA	10080
	ATTAGGAACA AGACAATGCA AGGAAAGGGT TAAATCATGC CCTTCAAACC ATAAGGGAT	10140
	TTTTTTAA TTAACCCAT ATAATGTGGT ATACTTCCA AACTGACTCT GGTATAGCAT	10200
	CACATGACAG ATTGCAGACT CCCTTACCTT AAGCATTCTT TTATACTGAC TTCAAGTCTT	10260
	AAGACAGAGC TGAACTCTT CAACCAGCTG CTAACTAAAG AATACCTAAA ACCCACCTGT	10320
10	GACTTGTAAAG TCTCTGCTTT GCCATGTCT GCCTTTCAAG GCTGACCCAA TGATACCTT	10380
	CCGTGTATTG ATTTATGATT TTTACCTACA ATTCCGTCT TCCTGAAACA TATAAAACCA	10440
	AATCATAACC CAACCACCTC AGGCACACTT TCTCAGGACC TCTTGAGACT ATTCTCCGG	10500
	CCATGGTCAT TCATATCGGC ACAGAATGAA ACCTCTTAA AATATTTCAG AGTTTTTTTC	10560
	TTTCTGTTAA CATTCTTTC CCTTGTATCA TTGCTGTTAT TAATTCAAG TATATATAAG	10620
15	CATACCTAAT TAAATACATT GTTGCTATTA TTCATTTTG AACAAACTAT TATCTGTTAA	10680
	ATCAACTAAG AATAAGACAA ATATGTTGGG TGCACTGGTG CATGCCTATA GTCTCAGCTA	10740
	CTCAGAGGCT GAGGCAGGAG GATTGCTTGA GCTCAGGAGT TTAAGACCAAG CCTAGGCAAC	10800
	TTAGCAAGAT CATGCTCTT AAAAAAAA AAAGAAAGAA AGAAAAACAA AGTTTTAGGA	10860
	GGCTGAGGCA GGAGTATCAC TTGAACCCAG GACGCAGAGG TTGCAGTGAG CCGAGATCGT	10920
20	GCCATTATAC TCCAGCCTGG GCAACAGAGT GAGACTCTGT CTAAAAAAA AAAAGAAAA	10980
	GAAAAGAAAA GAAAAAAA GTTTTATTT TACCTTCACT TATTCTTCT TGATGTTCT	11040
	TCCTTATGT AGGTACAAGG TTCTGACCTA TGTTATTTTC TTTTCTCTA AAGAACTTCA	11100
	AAAGTTTCTT GCAAGGCAGG TCTACTGGCA ATGAATTCCC TCAATTTTG CTTGACAAAG	11160
	TCTTATTTTC TGCTTCACTA TTGATGGATA ATTCACAAG AGTGTCTT TTGTAGATT	11220
25	ACTCTTCTTA TCCTTCCCTT CAGAAATATT CTTGACCAA CTATTGGTC CCAGGTACTG	11280
	CACTAGAGCT TTACTTCTAG TTAATTCCA CAGCAATTCT GAGAGGTAGG TAGGTATTAT	11340
	ATTCCTAGAT GCAAACTCAG AATTCAAGAAG GTAAAGTGTAT GAGACTGAAG GCACACAGCA	11400
	AGTAAGTGGC AGAACCTAGA TAAACACTCA TTCTTAAAC TTTGGCTTCC TTCTCTTTC	11460
	TTTAATGGAT TCAGTTACTT CTTCTCACCC ACTCACCTTT ATCAATTAC ATTCAGATA	11520
30	AAAGTCTTCA TGTTGGCANC TCAATGTGCC TTAACAAGAA GATGCCACA AGAAGGGTT	11580
	GATCATCGGG ACAGCAAAGT GTCTCTCAA GAGAAAAACT GTGAACCTGT GGTAGGTTAA	11640
	GATCCTTCA AAGGGTATT TCATGAATGG CTGTTTTAA CTCAAGTGAATACAATTATT	11700
	TCCATTAAA AAGCAAGGAC AATGTGAATG TACTCATTGC CACTGAACCA TATACACCTA	11760
	AAAATGGTTA AAATGGCAAC TTTATGTGT ATTTATGAG AATAAAAAT AAATAATAAT	11820
35	AAAAAAACAAG GGAAGTACAG ATATTTCTT AATTGTGTTG TCACATACCC AGTGTCTTCA	11880
	GGGTCAATAA TGAGAGCCCT ACATGTAAGA TTCAAAGGAA GAATTAGTC CTGGATACAA	11940
	TATTCTTTA TGTTTTAGT TATATTGCC TTTTAATGG ATGCAGATAT ATACAGAGGG	12000
	AAGGGATAAA GTACCTATTA TTTATTGTAT AGAGCTGTGC TGTCTGATGG CTTAGCCACT	12060
	AGTCACATGG TGCTATTGAA CACTTAAAC ACAGGAGTTT GAAATAAGCA TGTATTATAA	12120
40	TACATATCAT ATTCAAAAA TATTAGTATG TAGAAAAGAA GATAAATGGT TCATTAATGA	12180
	TTTTATATT GATTACACCTT GAAATAAATA TTCTGAAAAT ATTAGGTTAA ACAAAATATT	12240

5	TTAAGATTAA TTTTACATGT TTCTTCTTT AAATGTAGCT ACTAGAAATT TAAAGATTAC	12300
	ATATGGCTGG GCATGGTGGC TCACACCTGT AATCCCAGCA CTTGGGAGG CCGAGGTGGG	12360
	TGGATCACCT GATCTCAGGA GCTCGAGACC AGCCTGGCAA ACATGGTGAA ATCCTATCTT	12420
	TACTAAAAT ACAAAAATTA GCCAAGCGTG GTGGTGCATG CCTGTAATCC CAGCTACTTG	12480
	GGACGCTGAG GCAGGAGAAT CACTTGAACC CGGGAGGTGG AGGTTGCAGT GAGCCGAGAT	12540
10	AGTGCCACTG CACTCCAGCC TGGGAGACAA GAGCAAAACT CCATCTAAA AATAAATAAA	12600
	TAAAATAAAA TTACATAAGT GGCTTGACCC ATATTCTAT TGGACAGCAC TAGTACATAT	12660
	ACAACACAGC ATAATGGTTG AGAGCACTGA CTCTGGAGCC AAATTACTGT GTTGATTCT	12720
	TAGCTCCACA ACTTACTAGT TGTGTGACCA TGGGCAAGCG AGTTAACCTC TCTGTGCC	12780
	AGTTTCCCCT TCTGTAACAT GAAAATAATA AAAACACTCC CCAGAATTGT TGTGAGCATT	12840
15	AAATGAAGCC CTGACACATT TGTTCTGGAT ACAATATCCT CTTGTTTAT ATTTGGTAGT	12900
	ATCAATGTGC CTTAGACAC AATTACAACG ATCTCTGTGG TAAAGATGCA ATGTATATGG	12960
	TGTCTATAAA TAGCATTCAA TGATTCGTTA GTTAGGGCTT GAGACTTTA CTGTCATGGA	13020
	AAATCTAGGT ATAGCTAAGC TTTGAGATT TTGGGAACCTC CTTAACCTA TTTTCTCTA	13080
	CTCTTGCCCC CAACAATCAG CCTATATACT TGTGAAATT AACAATTACT TCACTGGCA	13140
20	GAAATTATAT GGGAACACTT AGAAATTTCAGT GTCCACAGGG AAAGTATAAA TATGTTAAT	13200
	ATTTTAACCT AATCCCTTCC TAGAAACACA TACACTGTTG CCAAGCCCAT ATTCTCCCTT	13260
	TCTTGTTCACCA ACAGTTCCACC ATGCTCCACC TGCTTATGAG AAACCTCTG CAGAACAGTC	13320
	ACCACCACTT TATTACACCTT AAGAGCCAGC GAGACACCTG AGACATGCTG AAATTATTC	13380
	TCTCACACTT TTGCTTGAAT TTAATACAGA CATCTAATGT TCTCCTTGG AATGGTAG	13440
25	GAAAAATGCA AGCCATCTCT AATAATAAGT CAGTGTAAA ATTTAGTAG GTCCGCTAGC	13500
	AGTACTAATC ATGTGAGGAA ATGATGAGAA ATATTAAATT GGGAAAACCTC CATCAATAAA	13560
	TGTTGCAATG CATGATAAAA AAAAA	13585

(2) INFORMATION FOR SEQUENCE ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 648 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

35	AGCTGCCGTC CGGACTCTT TTCTCTACT GAGATTACATC TGTGTGAAAT ATGAGTTGGC	60
	GAGGAAGATC GACCTATCGG CCTAGACCAA GACGCTACGT AGAGCCTCCT GAAATGATTG	120
	GGCCTATGCG GCCCGAGCAG TTCAGTGATG AAGTGGAACCC AGCAACACCT GAAGAAGGGG	180
40	AACCAGCAAC TCAACGTCAG GATCCTGCAG CTGCTCAGGA GGGAGAGGAT GAGGGAGCAT	240
	CTGCAGGTCA AGGGCCGAAG CCTGAAGCTG ATAGCCAGGA ACAGGGTCAC CCACAGACTG	300

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5 CTGCAGGTCA AGGGCCGAAG CCTGAAGCTG ATAGCCAGGA ACAGGGTCAC CCACAGACTG 300
 GGTGTGAGTG TGAAGATGGT CCTGATGGGC AGGAGATGGA CCCGCCAAAT CCAGAGGGAGG 360
 TGAAAACGCC TGAAGAAGAG ATGAGGTCTC ACTATGTTGC CCAGACTGGG ATTCTCTGGC 420
 TTTAATGAA CAATTGCTTC TTAAATCTT CCCCACGGAA ACCTTGAGTG ACTGAAATAT 480
 CAAATGGCGA GAGACCGTTT AGTTCCATC ATCTGTGGCA TGTGAAGGGC AATCACAGTG 540
10 TTAAAAGAAG ACATGCTGAA ATGTTGCAGG CTGCTCCTAT GTTGGAAAAT TCTTCATTGA 600
 AGTTCTCCA ATAAAGCTTT ACAGCCTTCT GCAAAGAAAA AAAAAAAA 648

(2) INFORMATION FOR SEQUENCE ID NO: 53:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Ala Leu Ser Arg Lys Val Ala Glu Leu

5

25 (2) INFORMATION FOR SEQUENCE ID NO: 54:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
30 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Phe Leu Trp Gly Pro Arg Ala Leu Val

5

35 (2) INFORMATION FOR SEQUENCE ID NO: 55:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acid residues
 (B) TYPE: amino acid

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5 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Thr Leu Val Glu Val Thr Leu Gly Glu Val

10 5 10

(2) INFORMATION FOR SEQUENCE ID NO: 56:
(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

20 Ala Leu Ser Arg Lys Val Ala Glu Leu Val
5 10

25 (2) INFORMATION FOR SEQUENCE ID NO: 57:
(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

35 Ala Leu Val Glu Thr Ser Tyr Val Lys Val

5 10

40 (2) INFORMATION FOR SEQUENCE ID NO: 58:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acid residues

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5 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

10 Ser Thr Leu Val Glu Val Thr Leu Gly Glu Val
1 5 10

15 (2) INFORMATION FOR SEQUENCE ID NO: 59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
20 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Leu Val Glu Val Thr Leu Gly Glu Val
1 5

25

(2) INFORMATION FOR SEQUENCE ID NO: 60:
(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

35 Lys Met Val Glu Leu Val His Phe Leu
1 5

40 (2) INFORMATION FOR SEQUENCE ID NO: 61:

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5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Val Ile Phe Ser Lys Ala Ser Glu Tyr Leu

1 5 10

15

(2) INFORMATION FOR SEQUENCE ID NO: 62:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

25 Tyr Leu Gln Leu Val Phe Gly Ile Glu Val

1 5 10

30 (2) INFORMATION FOR SEQUENCE ID NO: 63:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
35 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Gln Leu Val Phe Gly Ile Glu Val Val

1 5

40 (2) INFORMATION FOR SEQUENCE ID NO: 64:
(i) SEQUENCE CHARACTERISTICS:

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5 (A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

10 Gln Leu Val Phe Gly Ile Glu Val Val Glu Val
1 5 10

15 (2) INFORMATION FOR SEQUENCE ID NO: 65:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
20 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Ile Ile Val Leu Ala Ile Ile Ala Ile
25 1 5

30 (2) INFORMATION FOR SEQUENCE ID NO: 66:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
35 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Lys Ile Trp Glu Glu Leu Ser Met Leu Glu Val
1 5 10

40

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5 (2) INFORMATION FOR SEQUENCE ID NO: 67:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ala Leu Ile Glu Thr Ser Tyr Val Lys Val

1 5 10

15

20 (2) INFORMATION FOR SEQUENCE ID NO: 68:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

25

Leu Ile Glu Thr Ser Tyr Val Lys Val Leu

1 5 10

30

35 (2) INFORMATION FOR SEQUENCE ID NO: 69:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: M3-195.203 OR SEQ ID NO: 69:

Ile Met Pro Lys Ala Gly Leu Leu Ile

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(2) INFORMATION FOR SEQUENCE ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: M3-220.228 OR SEQ ID NO: 70:

10

Lys Ile Trp Glu Glu Leu Ser Val Leu

15

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(2) INFORMATION FOR SEQUENCE ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 14 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

25

Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser Ser

5

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(2) INFORMATION FOR SEQUENCE ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acid residues

(B) TYPE: amino acid

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp

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5 (2) INFORMATION FOR SEQUENCE ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Asp Val Lys Glu Ala Asp Pro Thr Gly His Ser Tyr

15 5 10

(2) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

25

GC	GGCGGTGG	CGGAGGCGGA	CACATTGGCG	TGAGACCTGG	GAGTACGTTG	TGCCAAATCA	60
TT	TGCCACTTG	CCACATGAGT	GTAAATGATG	GGGGATGCAA	GTATGTCTC	TGCCGATGGG	120
AA	AAAGCGATT	ATGGCCTGCG	AAGGTGACAG	CCATTATTCT	GTAACTTAG	GACTTAGAAA	180
30	TGACTTTCGG	GTGACAAGTA	AAATCTTGAT	CAGGAGATAC	CTAGGATTTG	CTTCAGTGAA	240
AT	ATAATTGAGC	CAGAACACGG	TTGGCACTGA	TTCTCGTTCC	CCATTTAATG	GGGTTTTGGT	300
CT	CTAGTGCTTC	CAAGGTTACA	CTTCCAGAAA	TGTCTTTTT	TTTCACACT	AAAAAAAAAAA	360
AA	AAAAGAATCA	GCTGTAAAAA	GGCATGTAAG	GCTGTAACTC	AAGGAAAGAT	CTGGCAAGCA	420
40	GCCCTGTGAT	AGTAAATTAT	GGTCGTGTTG	AGGGAATGCT	TTCCAGCAAT	TCAGTAGACA	480
GT	GTGCTCAGCT	GCAATGCAAA	AGCCCAGGTC	CTTGTCTTG	TCTGCCACTG	GCCTCTCATG	540
CC	CCTCAGTTTC	CCCATCTGTG	AAACAATGGG	GATTGGACCA	AATATCTGAA	ATCCCATGGT	600
CT	TATAGGCCCTT	CAGGATTACC	TGCTGCATT	GTGCTAAAGT	TTGCCACTGT	TTCTCACTGT	660
CA	CAGCTGTTGT	AATAACAAGG	ATTTCTTTT	GTTTAAATG	TAGGTTTTGG	CCCGAACCGC	720
GA	GA	AAAAATAAGA	GAAGAAAGGA	ATATTTCTA	GCTGTGCAA	TCCTCTCCCT	780
AG	AGAGGAAAAG	TTAATTGTTG	TGTTGTTTA	ATACTGTTT	TTCCCCTGTA	GATTCTGTAT	840
AC	ACTTCAATCC	CCTACTCCCC	CAAAACAGTT	GAAGCCCAGC	CCACTCTTAA	TGGGCTTATT	900

5	CAACATTGT GTAATT CATT AATGCT CATA ATAACCT CAT GAGAAAGCAA CTAGTTGAT	960
	TTTATGTCAG TTTGGAAGCT GAAGATCCAA ACGAGGCATT CTGTGAGATC TATGGAGAGA	1020
	TTGGTACAAA CACTGAATAC ATGTAAATT AACTCAGGGT AGACCCATT TGTGGTTAAA	1080
	ATAGGGATAT TTCCCTTTTT TTTCCTTTTT TTTTGACTGT TTCTTAATCA GTGCCATGCC	1140
	AGGAAAATAG GGATGTTCC TTCCCAGAGA TCTGTGTGTC TTTTTCAGA AACGTCTGTG	1200
10	ACAGGCCAT CAATTTGAA ATATTTGGTT TTTGAGCCTG TCACTCTAAA CCAGCGTTA	1260
	ACGTTCAAAA GGCAAATAAC TGATGACCAG GCGGCACATT GTTCTGCTCC GTGAGTGTCT	1320
	GGCACTGGGA AAGGTGTAGA TTGTCTAGAA TGACAGCAAT TCCGACGCC CAGTCAGTCC	1380
	TGCGTGTATTG TGGCGAGGGC GCGTCTGGCA CCGGGAAAGGT GTAGATCATC TAGAATGAGC	1440
	GCGATTCCGA CGCCCCGGTC AGTCCTGCCT GATTGGCGAG GGTGCATCTG TCGTGAGAAT	1500
15	TCCCAGTTCT GAAGAGAGCA AGGAGACTGA TCCCGCGTAG TCCAAGGCAT TGGCTCCCCT	1560
	GTTGCTCTTC CTTGTGGAGC TCCCCCTGCC CCACCTCCCTC CTGCCTGCAT CTTCAGAGCT	1620
	GCCTCTGAAG CTCGCTTGGT CCCTAGCTCA CACTTTCCCT GCGGCTGGGA AGGTAATTGA	1680
	ATACTCGAGT TTAAAAGGAA AGCACATCCT TTTAAACCAA AACACACCTG CTGGGCTGT	1740
	AACAGCTTT AGTGACATTA CCATCTACTC TGAAAATCTA ACAAAGGAGT GATTTGTGCA	1800
20	GTTGAAAGTA GGATTTGCTT CATAAAAGTC ACAATTGAA TTCATTTTG CTTTAAATC	1860
	CAGCCAACCT TTTCTGTCTT AAAAGGAAAA AAAAAA	1896

25 (2) INFORMATION FOR SEQUENCE ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Glu Glu Lys Leu Ile Val Val Leu Phe

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(2) INFORMATION FOR SEQUENCE ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

5 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: nucleic acid
 (ix) FEATURE:
 (A) NAME/KEY: DAGE
 (D) OTHER INFORMATION: Xaa is Arg when V is C or A or Gly
 10 when V is G
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

	VGA CTG AGA CCT AGA AAT CCA AGC GTT GGA GGT CCT GAG GCC AGC CTA	48
15	Xaa Leu Arg Pro Arg Asn Pro Ser Val Gly Gly Pro Glu Ala Ser Leu	
	1 5 10 15	
	AGT TTC CGC AAA ATG GAA CGA AGG CGT TTG CGG GGT TCC ATT CAG AGC	596
	Ser Arg Phe Lys Met Glu Arg Arg Leu Arg Gly Ser Ile Gln Ser	
20	20 25 30	
	CGA TAC ATC AGC ATG AGT GTG TGG ACA AGC CCA CGG AGA CTT GTG GAG	144
	Arg Tyr Ile Ser Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu	
	35 40 45	
25	CTG GCA GGG CAG AGC CTG CTG AAG GAT GAG GCC CTG GCC ATT GCC GCC	192
	Leu Ala Gly Gln Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala	
	50 55 60	
30	CTG GAG TTG CTG CCC AGG GAG CTC TTC CCG CCA CTC TTC ATG GCA GCC	240
	Leu Glu Leu Leu Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala	
	65 70 75 80	
35	TTT GAC GGG AGA CAC AGC CAG ACC CTG AAG GCA ATG GTG CAG GCC TGG	288
	Phe Asp Gly Arg His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp	
	85 90 95	
40	CCC TTC ACC TGC CTC CCT CTG GGA GTG CTG ATG AAG GGA CAA CAT CTT	336
	Pro Phe Thr Cys Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu	
	100 105 110	

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5	CAC CTG GAG ACC TTC AAA GCT GTG CTT GAT GGA CTT GAT GTG CTC CTT	384		
	His Leu Glu Thr Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu			
	115	120	125	
10	GCC CAG GAG GTT CGC CCC AGG AGG TGG AAA CTT CAA GTG CTG GAT TTA	432		
	Ala Gln Glu Val Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu			
	130	135	140	
15	CGG AAG AAC TCT CAT CAG GAC TTC TGG ACT GTA TGG TCT GGA AAC AGG	480		
	Arg Lys Asn Ser His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg			
	145	150	155	160
20	GCC AGT CTG TAC TCA TTT CCA GAG CCA GAA GCA GCT CAG CCC ATG ACA	528		
	Ala Ser Leu Tyr Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr			
	165	170	175	
25	AAG AAG CGA AAA GTA GAT GGT TTG AGC ACA GAG GCA GAG CAG CCC TTC	576		
	Lys Lys Arg Lys Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe			
	180	185	190	
30	ATT CCA GTA GAG GTG CTC GTA GAC CTG TTC CTC AAG GAA GGT GCC TGT	624		
	Ile Pro Val Glu Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys			
	195	200	205	
35	GAT GAA TTG TTC TCC TAC CTC ATT GAG AGA GTG AAG CGA AAG AAA AAT	672		
	Asp Glu Leu Phe Ser Tyr Leu Ile Glu Arg Val Lys Arg Lys Lys Asn			
	210	215	220	
40	GTA CTA CGG CTG TGC TGT AAG AAG CTG AAG ATT TTT GCA ATG CCC ATG	720		
	Val Leu Arg Leu Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met			
	225	230	235	240
	CAG GAT ATC AAG ATG ATC CTG AAA ATG GTG CAG CTG GAC TCT ATT GAA	768		
	Gln Asp Ile Lys Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu			
	245	250	255	
	GAT TTG GAA GTG ACT TGT ACC TGG AAG CTA CCC ACC TTG GCG AAA TTT	816		

5	Asp Leu Glu Val Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe			
	260	265	270	
	TCT CCT TAC CTG GGC CAG ATG ATT AAT CTG CGT AGA CTC CTC CTC TCC			864
10	Ser Pro Tyr Leu Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser			
	275	280	285	
	CAC ATC CAT GCA TCT TCC TAC ATT TCC CCG GAG AAG GAA GAG AGT ATA			912
	His Ile His Ala Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Ser Ile			
	290	295	300	
15	TCG CCC AGT TCA CCT CTC AGT TCC TCA GTC TGC AGT GCC TGC AGG CTC			960
	Ser Pro Ser Ser Pro Leu Ser Ser Ser Val Cys Ser Ala Cys Arg Leu			
	305	310	315	320
20	TCT ATG TGG ACT CTT TAT TTT TCC TTA GAG GCC GCC TGG ACT CAG TTG			1008
	Ser Met Trp Thr Leu Tyr Phe Ser Leu Glu Ala Ala Trp Thr Gln Leu			
	325	330	335	
25	CTC AGG CAC GTG ATG AAC CCC TTG GAA ACC CTC TCA ATA ACT AAC TGC			1056
	Leu Arg His Val Met Asn Phe Leu Glu Thr Leu Ser Ile Thr Asn Cys			
	340	345	350	
30	CGG CTT TCG GAA GGG GAT GTG ATG CAT CTG TCC CAG AGT CCC AGC GTC			1104
	Arg Leu Ser Glu Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val			
	355	360	365	
35	AGT CAG CTA AGT GTC CTG AGT CTA AGT GGG GTC ATG CTG ACC GAT GTA			1152
	Ser Gln Leu Ser Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val			
	370	375	380	
40	AGT CCC GAG CCC CTC CAA GCT CTG CTG GAG AGA GCA TCT GCC ACC CTC			1200
	Ser Pro Glu Pro Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu			
	385	390	395	400
	CAG GAC CTG GTC TTT GAT GAG TGT GGG ATC ACG GAT GAT CAG CTC CTT			1248
	Gln Asp Leu Val Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu			

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410

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GCC CTC CTG CCT TCC CTG AGC CAC TGC TCC CAG CTT ACA ACC TTA AGC 1296
 Ala Leu Leu Pro Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser
 420 425 430

10

TTC TAC GGG AAT TCC ATC TCC ATA TCT GCC TTG CAG AGT CTC CTG CAG 1344
 Phe Tyr Gly Asn Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln
 435 440 445

15

CAC CTC ATC GGG CTG AGC AAT CTG ACC CAC GTG CTG TAT CCT GTC CCC 1392
 His Leu Ile Gly Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro
 450 455 460

20

CTG GAG AGT TAT GAG GAC ATC CAT GGT ACC CTC CAC CTG GAG AGG CTT 1440
 Leu Glu Ser Tyr Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu
 465 470 475 480

25

GCC TAT CTG CAT GCC AGG CTC AGG GAG TTG CTG TGT GAG TTG GGG CGG 1488
 Ala Tyr Leu His Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg
 485 490 495

30

CCC AGC ATG GTC TGG CTT AGT GCA ACC CCT GTC CTC ACT GTG GGG ACA 1536
 Pro Ser Met Val Trp Leu Ser Ala Thr Pro Val Leu Thr Val Gly Thr
 500 505 510

GAA CCT TCT ATG ACC CGG
 Glu Pro Ser Met Thr Arg
 515

1554

We claim:

1. Composition of matter comprising:
 - (i) a tumor rejection antigen precursor or a tumor rejection antigen, and at least one of:
 - (ii) a pharmaceutically acceptable adjuvant, and a T or B cell growth factor.
2. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a MAGE protein.
3. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a BAGE protein.
4. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a GAGE protein.
5. The composition of claim 1, wherein said tumor rejection antigen is derived from a MAGE protein.
6. The composition of matter of claim 5, wherein said MAGE protein is MAGE-1, MAGE-2, or MAGE-3.
7. The composition of matter of claim 6, wherein said tumor rejection antigen consists of one of SEQ ID NO: 1 through SEQ ID NO: 5.
8. The composition of matter of claim 1, wherein said pharmaceutically acceptable adjuvant is a substantially pure saponin derived from Quillaja saponaria.
9. The composition of matter of claim 8, wherein said substantially pure saponin is selected from the group consisting of QA-7, QA-21, QA-17, and QA-18.
10. The composition of matter of claim 1, wherein said pharmaceutically acceptable adjuvant is MTP-MF59.

11. Method for stimulating an immune response in a subject comprising administering the composition of matter of claim 1 to said subject in an amount sufficient to provoke an immune response to said tumor rejection antigen precursor or tumor rejection antigen.

12. The method of claim 11, wherein said immune response comprises proliferation of T cells specific for complexes of said tumor rejection antigen and a major histocompatibility complex molecule to which said tumor rejection antigen binds.

13. The method of claim 11, wherein said T cells are cytolytic T cells.

14. The method of claim 11, wherein said immune response comprises production of antibodies against said tumor rejection antigen precursor or tumor rejection antigen.

15. The composition of claim 1, in intravenous form.

16. The composition of claim 1, in the form of a liposome.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/12463

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :A61K 38/00, 39/385, 45/00, 45/05; C07K 7/00, 14/00, 14/82
 US CL :424/185.1, 193.1, 277.1; 530/300, 350, 395, 868

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/185.1, 193.1, 277.1; 530/300, 350, 395, 868

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Examiner's tumor rejection file references

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Automated Patent System and DIALOG (file = BIOCHEM). Key words: MAGE, tumor rejection antigen?

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US, A, 5,342,774 (BOON ET AL) 30 August 1994.	1-16
A, P	US, A, 5,405,940 (BOON ET AL.) 11 April 1995.	1-16
A, E	US, A, 5,462,871 (BOON-FALLEUR ET AL) 31 October 1995.	1-16
Y	R. W. Ellis (ed.) "Vaccines: New Approaches To Immunological Problems", published 1992 by Butterworth-Heinemann (Stoneham, MA), pages 431-449, see entire document.	1-16
Y	Vaccine, Volume 11, Issue 3, issued 1993, Gupta et al., "Adjuvants - a balance between toxicity and adjuvanticity", pages 293-306, see entire document.	1-16

Further documents are listed in the continuation of Box C. See patent family annex.

•	Special categories of cited documents:	•	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A	document defining the general state of the art which is not considered to be part of particular relevance	*T*	
E	earlier document published on or after the international filing date	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L	document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O	document referring to an oral disclosure, use, exhibition or other means	*&*	document member of the same patent family
P	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

03 JANUARY 1996

Date of mailing of the international search report

09 FEB 1996

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/12463

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Immunology Today, Volume 14, No. 6, issued 1993, Hadden, "Immunostimulants", pages 275-280, see entire document.	1-16